

10/581551

AP20 Rec'd PCT/PTO 02 JUN 2006

SEQUENCE LISTING

<110> RIKEN

<120> Fluorescent protein

<130> A41869A

<160> 81

<210> 1

<211> 218

<212> PRT

<213> Fungia sp.

<400> 1

Met Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp

1 5 10 15

Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly

20 25 30

Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala

35 40 45

Lys Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe

50 55 60

Cys Tyr Gly His Arg Pro Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp

65 70 75 80

Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu

85 90 95

Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu

100 105 110

Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe

115 120 125

Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro

130	135	140
Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val		
145	150	155
Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe		160
	165	170
Lys Thr Thr Tyr Lys Ala Ala Lys Lys Ile Leu Lys Met Pro Gly Ser		175
	180	185
His Tyr Ile Ser His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr		190
	195	200
Glu Leu Val Glu Asp Ala Val Ala His Ser		205

210

215

<210> 2

<211> 657

<212> DNA

<213> Fungia sp.

<400> 2

atg gtg agt gtg att aaa cca gag atg aag atg agg tac tac atg gac 48
Met Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp
1 5 10 15
ggc tcc gtc aat ggg cat gag ttc aca att gaa ggt gaa ggc aca ggc 96
Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly
20 25 30
aga cct tac gag gga cat caa gag atg aca cta cgc gtc aca atg gcc 144
Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala
35 40 45
aag ggc ggg cca atg cct ttc gcg ttt gac tta gtg tca cac gtg ttc 192
Lys Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe

50	55	60	
tgt tac ggc cac aga cct ttt act aaa tat cca gaa gag ata cca gac	240		
Cys Tyr Gly His Arg Pro Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp			
65	70	75	80
tat ttc aaa caa gca ttt cct gaa ggc ctg tca tgg gaa agg tcg ttg	288		
Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu			
85	90	95	
gag ttc gaa gat ggt ggg tcc gct tca gtc agt gcg cat ata agc ctt	336		
Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu			
100	105	110	
aga gga aac acc ttc tac cac aaa tcc aaa ttt act ggg gtt aac ttt	384		
Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe			
115	120	125	
cct gcc gat ggt cct atc atg caa aac caa agt gtt gat tgg gag cca	432		
Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro			
130	135	140	
tca acc gag aaa att act gcc agc gac gga gtt ctg aag ggt gat gtt	480		
Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val			
145	150	155	160
acg atg tac cta aaa ctt gaa gga ggc ggc aat cac aaa tgc caa ttc	528		
Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe			
165	170	175	
aag act act tac aag gcg gca aaa aag att ctt aaa atg cca gga agc	576		
Lys Thr Thr Tyr Lys Ala Ala Lys Lys Ile Leu Lys Met Pro Gly Ser			
180	185	190	
cat tac atc agc cat cgc ctc gtc agg aaa acc gaa ggc aac att act	624		
His Tyr Ile Ser His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr			

195	200	205	
gag ctg gta gaa gat gca gta gct cat tcc tga			657
Glu Leu Val Glu Asp Ala Val Ala His Ser			
210	215		
<210> 3			
<211> 218			
<212> PRT			
<213> Fungia sp.			
<400> 3			
Met Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp			
1	5	10	15
Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly			
	20	25	30
Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala			
	35	40	45
Lys Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe			
50	55	60	
Cys Tyr Gly His Arg Cys Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp			
65	70	75	80
Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu			
	85	90	95
Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu			
100	105	110	
Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe			
115	120	125	
Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro			
130	135	140	

Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Asp  
 145 150 155 160  
 Thr Leu Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Met  
 165 170 175  
 Lys Thr Thr Tyr Lys Ala Ala Lys Lys Ile Leu Lys Met Pro Gly Ser  
 180 185 190  
 His Tyr Ile Ser His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr  
 195 200 205  
 Glu Leu Val Glu Asp Ala Val Ala His Ser  
 210 215

<210> 4

<211> 657

<212> DNA

<213> *Fungia* sp.

<400> 4

atg gtg agt gtg att aaa cca gag atg aag atg agg tac tac atg gac 48  
 Met Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp  
 1 5 10 15  
 ggc tcc gtc aat ggg cat gag ttc aca att gaa ggt gaa ggc aca ggc 96  
 Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly  
 20 25 30  
 aga cct tac gag gga cat caa gag atg aca cta cgc gtc aca atg gcc 144  
 Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala  
 35 40 45  
 aag ggc ggg cca atg cct ttc gcg ttt gac tta gtg tca cac gtg ttc 192  
 Lys Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe  
 50 55 60

tgc tac ggc cac aga tgt ttt act aaa tat cca gaa gag ata cca gac 240  
 Cys Tyr Gly His Arg Cys Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp  
 65 70 75 80  
 tat ttc aaa caa gca ttt cct gaa ggc ctg tca tgg gaa agg tcg ttg 288  
 Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu  
 85 90 95  
 gag ttc gaa gat ggt ggg tcc gct tca gtc agt gcg cat ata agc ctt 336  
 Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu  
 100 105 110  
 aga gga aac acc ttc tac cac aaa tcc aaa ttt act ggg gtt aac ttt 384  
 Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe  
 115 120 125  
 cct gcc gat ggt cct atc atg caa aac caa agt gtt gat tgg gag cca 432  
 Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro  
 130 135 140  
 tca acc gag aaa att act gcc agc gac gga gtt ctg aag ggt gat gac 480  
 Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Asp  
 145 150 155 160  
 acg ttg tac cta aaa ctt gaa gga ggc ggc aat cac aaa tgc caa atg 528  
 Thr Leu Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Met  
 165 170 175  
 aag act act tac aag gcg gca aaa aag att ctt aaa atg cca gga agc 576  
 Lys Thr Thr Tyr Lys Ala Ala Lys Lys Ile Leu Lys Met Pro Gly Ser  
 180 185 190  
 cat tac atc agc cat cgc ctc gtc agg aaa acc gaa ggc aac att act 624  
 His Tyr Ile Ser His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr  
 195 200 205

gag ctg gta gaa gat gca gta gct cat tcc taa

657

Glu Leu Val Glu Asp Ala Val Ala His Ser

210

215

<210> 5

<211> 218

<212> PRT

<213> Fungia sp.

<400> 5

Met Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp

1

5

10

15

Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly

20

25

30

Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala

35

40

45

Lys Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe

50

55

60

Gly Tyr Gly His Arg Gly Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp

65

70

75

80

Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu

85

90

95

Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu

100

105

110

Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe

115

120

125

Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro

130

135

140

Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Asp

145	150	155	160
Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Met			
	165	170	175
Lys Thr Thr Tyr Lys Ala Ala Lys Lys Ile Leu Lys Met Pro Gly Ser			
	180	185	190
His Tyr Ile Ser His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr			
	195	200	205
Glu Leu Val Glu Asp Ala Val Ala His Ser			

210

215

<210> 6

<211> 657

<212> DNA

<213> *Fungia* sp.

<400> 6

atg gtg agt gtg att aaa cca gag atg aag atg agg tac tac atg gac 48
Met Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp
1 5 10 15
ggc tcc gtc aat ggg cat gag ttc aca att gaa ggt gaa ggc aca ggc 96
Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly
20 25 30
aga cct tac gag gga cat caa gag atg aca cta cgc gtc aca atg gcc 144
Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala
35 40 45
aag ggc ggg cca atg cct ttc gcg ttt gac tta gtg tca cac gtg ttc 192
Lys Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe
50 55 60
ggg tac ggc cac aga ggt ttt act aaa tat cca gaa gag ata cca gac 240



Gly Tyr Gly His Arg Gly Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp  
 65 70 75 80  
 tat ttc aaa caa gca ttt cct gaa ggc ctg tca tgg gaa agg tcg ttg 288  
 Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu  
 85 90 95  
 gag ttc gaa gat ggt ggg tcc gct tca gtc agt gcg cat ata agc ctt 336  
 Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu  
 100 105 110  
 aga gga aac acc ttc tac cac aaa tcc aaa ttt act ggg gtt aac ttt 384  
 Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe  
 115 120 125  
 cct gcc gat ggt cct atc atg caa aac caa agt gtt gat tgg gag cca 432  
 Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro  
 130 135 140  
 tca acc gag aaa att act gcc agc gac gga gtt ctg aag ggt gat gat 480  
 Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Asp  
 145 150 155 160  
 acg atg tac cta aaa ctt gaa gga ggc ggc aat cac aaa tgc caa atg 528  
 Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Met  
 165 170 175  
 aag act act tac aag gcg gca aaa aag att ctt aaa atg cca gga agc 576  
 Lys Thr Thr Tyr Lys Ala Ala Lys Lys Ile Leu Lys Met Pro Gly Ser  
 180 185 190  
 cat tac atc agc cat cgc ctc gtc agg aaa acc gaa ggc aac att act 624  
 His Tyr Ile Ser His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr  
 195 200 205  
 gag ctg gta gaa gat gca gta gct cat tcc taa 657

Glu Leu Val Glu Asp Ala Val Ala His Ser

210

215

<210> 7

<211> 218

<212> PRT

<213> Fungia sp.

<400> 7

Met Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp

1

5

10

15

Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly

20

25

30

Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala

35

40

45

Lys Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe

50

55

60

Ala Tyr Gly His Arg Gly Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp

65

70

75

80

Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu

85

90

95

Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu

100

105

110

Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe

115

120

125

Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro

130

135

140

Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val

145

150

155

160

Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe

165

170

175

Lys Thr Thr Tyr Lys Ala Ala Lys Lys Ile Leu Lys Met Pro Gly Ser

180

185

190

His Tyr Ile Ser His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr

195

200

205

Glu Leu Val Glu Asp Ala Val Ala His Ser

210

215

<210> 8

<211> 657

<212> DNA

<213> Fungia sp.

<400> 8

atg gtg agt gtg att aaa cca gag atg aag atg agg tac tac atg gac 48

Met Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp

1

5

10

15

ggc tcc gtc aat ggg cat gag ttc aca att gaa ggt gaa ggc aca ggc 96

Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly

20

25

30

aga cct tac gag gga cat caa gag atg aca cta cgc gtc aca atg gcc 144

Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala

35

40

45

aag ggc ggg cca atg cct ttc gcg ttt gac tta gtg tca cac gtg ttc 192

Lys Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe

50

55

60

gct tac ggc cac aga ggt ttt act aaa tat cca gaa gag ata cca gac 240

Ala Tyr Gly His Arg Gly Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp

65	70	75	80
tat ttc aaa caa gca ttt cct gaa ggc ctg tca tgg gaa agg tcg ttg 288			
Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu			
85	90	95	
gag ttc gaa gat ggt ggg tcc gct tca gtc agt gcg cat ata agc ctt 336			
Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu			
100	105	110	
aga gga aac acc ttc tac cac aaa tcc aaa ttt act ggg gtt aac ttt 384			
Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe			
115	120	125	
cct gcc gat ggt cct atc atg caa aac caa agt gtt gat tgg gag cca 432			
Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro			
130	135	140	
tca acc gag aaa att act gcc agc gac gga gtt ctg aag ggt gat gtt 480			
Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val			
145	150	155	160
acg atg tac cta aaa ctt gaa gga ggc ggc aat cac aaa tgc caa ttc 528			
Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe			
165	170	175	
aag act act tac aag gcg gca aaa aag att ctt aaa atg cca gga agc 576			
Lys Thr Thr Tyr Lys Ala Ala Lys Lys Ile Leu Lys Met Pro Gly Ser			
180	185	190	
cat tac atc agc cat cgc ctc gtc agg aaa acc gaa ggc aac att act 624			
His Tyr Ile Ser His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr			
195	200	205	
gag ctg gta gaa gat gca gta gct cat tcc taa 657			
Glu Leu Val Glu Asp Ala Val Ala His Ser			

210  
 215  
 <210> 9  
 <211> 218  
 <212> PRT  
 <213> Fungia sp.  
 <400> 9  
 Met Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp  
 1 5 10 15  
 Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly  
 20 25 30  
 Arg Pro Tyr Glu Gly His Gln Glu Leu Thr Leu Arg Val Thr Met Ala  
 35 40 45  
 Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe  
 50 55 60  
 Cys Tyr Gly His Lys Pro Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp  
 65 70 75 80  
 Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu  
 85 90 95  
 Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu  
 100 105 110  
 Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe  
 115 120 125  
 Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro  
 130 135 140  
 Trp Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val  
 145 150 155 160  
 Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe

	165	170	175
Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp			
	180	185	190
His Tyr Ile Ser His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr			
	195	200	205
Glu Leu Val Glu Asp Ala Val Ala His Ser			

210  
<210> 10

<211> 657

<212> DNA

<213> Fungia sp.

<400> 10

atg gtg agt gtg att aaa cca gag atg aag atg agg tac tac atg gac 48
Met Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp
1 5 10 15
ggc tcc gtc aat ggg cat gag ttc aca att gaa ggt gaa ggc aca ggc 96
Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly
20 25 30
aga cct tac gag gga cat caa gag ctg aca cta cgc gtc aca atg gcc 144
Arg Pro Tyr Glu Gly His Gln Glu Leu Thr Leu Arg Val Thr Met Ala
35 40 45
gag ggc ggg cca atg cct ttc gcg ttt gac tta gtg tca cac gtg ttc 192
Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe
50 55 60
tgt tac ggc cac aaa cct ttt act aaa tat cca gaa gag ata cca gac 240
Cys Tyr Gly His Lys Pro Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp
65 70 75 80

tat ttc aaa caa gca ttt cct gaa ggc ctg tca tgg gaa agg tcg ttg 288  
 Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu  
                     85                    90                    95  
 gag ttc gaa gat ggt ggg tcc gct tca gtc agt gcg cat ata agc ctt 336  
 Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu  
                     100                    105                    110  
 aga gga aac acc ttc tac cac aaa tcc aaa ttt act ggg gtt aac ttt 384  
 Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe  
                     115                    120                    125  
 cct gcc gat ggt cct atc atg caa aac caa agt gtt gat tgg gag cca 432  
 Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro  
                     130                    135                    140  
 tgg acc gag aaa att act gcc agc gac gga gtt ctg aag ggt gat gtt 480  
 Trp Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val  
 145                    150                    155                    160  
 acg atg tac cta aaa ctt gaa gga ggc ggc aat cac aaa tgc caa ttc 528  
 Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe  
                     165                    170                    175  
 aag act act tac aag gcg gca aaa gag att ctt gaa atg cca gga gac 576  
 Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp  
                     180                    185                    190  
 cat tac atc agc cat cgc ctc gtc agg aaa acc gaa ggc aac att act 624  
 His Tyr Ile Ser His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr  
                     195                    200                    205  
 gag ctg gta gaa gat gca gta gct cat tcc taa 657  
 Glu Leu Val Glu Asp Ala Val Ala His Ser  
                     210                    215

<210> 11

<211> 218

<212> PRT

<213> Fungia sp.

<400> 11

Met Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp

1 5 10 15

Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly

20 25 30

Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala

35 40 45

Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe

50 55 60

Cys Tyr Gly His Arg Gly Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp

65 70 75 80

Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu

85 90 95

Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu

100 105 110

Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe

115 120 125

Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro

130 135 140

Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val

145 150 155 160

Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe

165 170 175



Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp

180

185

190

His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr

195

200

205

Glu Leu Val Glu Asp Ala Val Ala His Ser

210

215

<210> 12

<211> 657

<212> DNA

<213> Fungia sp.

<400> 12

atg gtg agt gtg att aaa cca gag atg aag atg agg tac tac atg gac 48

Met Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp

1

5

10

15

ggc tcc gtc aat ggg cat gag ttc aca att gaa ggt gaa ggc aca ggc 96

Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly

20

25

30

aga cct tac gag gga cat caa gag atg aca cta cgc gtc aca atg gcc 144

Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala

35

40

45

gag ggc ggg cca atg cct ttc gcg ttt gac tta gtg tca cac gtg ttc 192

Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe

50

55

60

tgt tac ggc cac aga ggt ttt act aaa tat cca gaa gag ata cca gac 240

Cys Tyr Gly His Arg Gly Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp

65

70

75

80

tat ttc aaa caa gca ttt cct gaa ggc ctg tca tgg gaa agg tcg ttg 288

Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu			
	85	90	95
gag ttc gaa gat ggt ggg tcc gct tca gtc agt gcg cat ata agc ctt 336			
Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu			
	100	105	110
aga gga aac acc ttc tac cac aaa tcc aaa ttt act ggg gtt aac ttt 384			
Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe			
	115	120	125
cct gcc gat ggt cct atc atg caa aac caa agt gtt gat tgg gag cca 432			
Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro			
	130	135	140
tca acc gag aaa att act gcc agc gac gga gtt ctg aag ggt gat gtt 480			
Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val			
	145	150	155
acg atg tac cta aaa ctt gaa gga ggc ggc aat cac aaa tgc caa ttc 528			
Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe			
	165	170	175
aag act act tac aag gcg gca aaa gag att ctt gaa atg cca gga gac 576			
Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp			
	180	185	190
cat tac atc ggc cat cgc ctc gtc agg aaa acc gaa ggc aac att act 624			
His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr			
	195	200	205
gag ctg gta gaa gat gca gta gct cat tcc taa 657			
Glu Leu Val Glu Asp Ala Val Ala His Ser			
	210	215	

<210> 13

<211> 218

<212> PRT

<213> Fungia sp.

<400> 13

Met	Val	Ser	Val	Ile	Lys	Pro	Glu	Met	Lys	Met	Arg	Tyr	Tyr	Met	Asp
1				5					10					15	
Gly	Ser	Val	Asn	Gly	His	Glu	Phe	Thr	Ile	Glu	Gly	Glu	Gly	Thr	Gly
			20					25						30	
Arg	Pro	Tyr	Glu	Gly	His	Gln	Glu	Met	Thr	Leu	Arg	Val	Thr	Met	Ala
			35					40					45		
Glu	Gly	Gly	Pro	Met	Pro	Phe	Ala	Phe	Asp	Leu	Val	Ser	His	Val	Phe
		50					55					60			
Cys	Tyr	Gly	His	Arg	Ala	Phe	Thr	Lys	Tyr	Pro	Glu	Glu	Ile	Pro	Asp
	65				70					75				80	
Tyr	Phe	Lys	Gln	Ala	Phe	Pro	Glu	Gly	Leu	Ser	Trp	Glu	Arg	Ser	Leu
			85						90					95	
Glu	Phe	Glu	Asp	Gly	Gly	Ser	Ala	Ser	Val	Ser	Ala	His	Ile	Ser	Leu
			100						105					110	
Arg	Gly	Asn	Thr	Phe	Tyr	His	Lys	Ser	Lys	Phe	Thr	Gly	Val	Asn	Phe
		115							120				125		
Pro	Ala	Asp	Gly	Pro	Ile	Met	Gln	Asn	Gln	Ser	Val	Asp	Trp	Glu	Pro
		130						135					140		
Ser	Thr	Glu	Lys	Ile	Thr	Ala	Ser	Asp	Gly	Val	Leu	Lys	Gly	Asp	Val
	145						150				155			160	
Thr	Met	Tyr	Leu	Lys	Leu	Glu	Gly	Gly	Gly	Asn	His	Lys	Cys	Gln	Phe
				165					170					175	
Lys	Thr	Thr	Tyr	Lys	Ala	Ala	Lys	Glu	Ile	Leu	Glu	Met	Pro	Gly	Asp

	180	185	190
His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr			
	195	200	205
Glu Leu Val Glu Asp Ala Val Ala His Ser			
	210	215	

<210> 14  
 <211> 657  
 <212> DNA  
 <213> Fungia sp.  
 <400> 14

atg gtg agt gtg att aaa cca gag atg aag atg agg tac tac atg gac 48
Met Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp
1 5 10 15
ggc tcc gtc aat ggg cat gag ttc aca att gaa ggt gaa ggc aca ggc 96
Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly
20 25 30
aga cct tac gag gga cat caa gag atg aca cta cgc gtc aca atg gcc 144
Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala
35 40 45
gag ggc ggg cca atg cct ttc gcg ttt gac tta gtg tca cac gtg ttc 192
Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe
50 55 60
tgt tac ggc cac aga gct ttt act aaa tat cca gaa gag ata cca gac 240
Cys Tyr Gly His Arg Ala Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp
65 70 75 80
tat ttc aaa caa gca ttt cct gaa ggc ctg tca tgg gaa agg tcg ttg 288
Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu

85	90	95	
gag ttc gaa gat ggt ggg tcc gct tca gtc agt gcg cat ata agc ctt 336			
Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu			
100	105	110	
aga gga aac acc ttc tac cac aaa tcc aaa ttt act ggg gtt aac ttt 384			
Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe			
115	120	125	
cct gcc gat ggt cct atc atg caa aac caa agt gtt gat tgg gag cca 432			
Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro			
130	135	140	
tca acc gag aaa att act gcc agc gac gga gtt ctg aag ggt gat gtt 480			
Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val			
145	150	155	160
acg atg tac cta aaa ctt gaa gga ggc ggc aat cac aaa tgc caa ttc 528			
Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe			
165	170	175	
aag act act tac aag gcg gca aaa gag att ctt gaa atg cca gga gac 576			
Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp			
180	185	190	
cat tac atc ggg cat cgc ctc gtc agg aaa acc gaa ggc aac att act 624			
His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr			
195	200	205	
gag ctg gta gaa gat gca gta gct cat tcc taa 657			
Glu Leu Val Glu Asp Ala Val Ala His Ser			
210	215		
<210> 15			
<211> 218			

<212> PRT

<213> Fungia sp.

<400> 15

Met	Val	Ser	Val	Ile	Lys	Pro	Glu	Met	Lys	Met	Arg	Tyr	Tyr	Met	Asp
1				5					10					15	
Gly	Ser	Val	Asn	Gly	His	Glu	Phe	Thr	Ile	Glu	Gly	Glu	Gly	Thr	Gly
			20					25						30	
Arg	Pro	Tyr	Glu	Gly	His	Gln	Glu	Met	Thr	Leu	Arg	Val	Thr	Met	Ala
			35					40						45	
Glu	Gly	Gly	Pro	Met	Pro	Phe	Ala	Phe	Asp	Leu	Val	Ser	His	Val	Phe
		50						55						60	
Cys	Tyr	Gly	His	Arg	Ser	Phe	Thr	Lys	Tyr	Pro	Glu	Glu	Ile	Pro	Asp
		65				70				75				80	
Tyr	Phe	Lys	Gln	Ala	Phe	Pro	Glu	Gly	Leu	Ser	Trp	Glu	Arg	Ser	Leu
			85						90					95	
Glu	Phe	Glu	Asp	Gly	Gly	Ser	Ala	Ser	Val	Ser	Ala	His	Ile	Ser	Leu
			100						105					110	
Arg	Gly	Asn	Thr	Phe	Tyr	His	Lys	Ser	Lys	Phe	Thr	Gly	Val	Asn	Phe
			115						120					125	
Pro	Ala	Asp	Gly	Pro	Ile	Met	Gln	Asn	Gln	Ser	Val	Asp	Trp	Glu	Pro
		130							135					140	
Ser	Thr	Glu	Lys	Ile	Thr	Ala	Ser	Asp	Gly	Val	Leu	Lys	Gly	Asp	Val
		145							150					155	
Thr	Met	Tyr	Leu	Lys	Leu	Glu	Gly	Gly	Gly	Asn	His	Lys	Cys	Gln	Phe
									165					170	
Lys	Thr	Thr	Tyr	Lys	Ala	Ala	Lys	Glu	Ile	Leu	Glu	Met	Pro	Gly	Asp
									180					185	
														190	

His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr

195

200

205

Glu Leu Val Glu Asp Ala Val Ala His Ser

210

215

<210> 16

<211> 657

<212> DNA

<213> Fungia sp.

<400> 16

atg gtg agt gtg att aaa cca gag atg aag atg agg tac tac atg gac 48

Met Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp

1

5

10

15

ggc tcc gtc aat ggg cat gag ttc aca att gaa ggt gaa ggc aca ggc 96

Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly

20

25

30

aga cct tac gag gga cat caa gag atg aca cta cgc gtc aca atg gcc 144

Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala

35

40

45

gag ggc ggg cca atg cct ttc gcg ttt gac tta gtg tca cac gtg ttc 192

Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe

50

55

60

tgt tac ggc cac aga tct ttt act aaa tat cca gaa gag ata cca gac 240

Cys Tyr Gly His Arg Ser Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp

65

70

75

80

tat ttc aaa caa gca ttt cct gaa ggc ctg tca tgg gaa agg tcg ttg 288

Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu

85

90

95

gag ttc gaa gat ggt ggg tcc gct tca gtc agt gcg cat ata agc ctt 336

Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu

100

105

110

aga gga aac acc ttc tac cac aaa tcc aaa ttt act ggg gtt aac ttt 384

Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe

115

120

125

cct gcc gat ggt cct atc atg caa aac caa agt gtt gat tgg gag cca 432

Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro

130

135

140

tca acc gag aaa att act gcc agc gac gga gtt ctg aag ggt gat gtt 480

Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val

145

150

155

160

acg atg tac cta aaa ctt gaa gga ggc ggc aat cac aaa tgc caa ttc 528

Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe

165

170

175

aag act act tac aag gcg gca aaa gag att ctt gaa atg cca gga gac 576

Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp

180

185

190

cat tac atc ggc cat cgc ctc gtc agg aaa acc gaa ggc aac att act 624

His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr

195

200

205

gag ctg gta gaa gat gca gta gct cat tcc taa

657

Glu Leu Val Glu Asp Ala Val Ala His Ser

210

215

<210> 17

<211> 218

<212> PRT



<213> Fungia sp.

<400> 17

Met	Val	Ser	Val	Ile	Lys	Pro	Glu	Met	Lys	Met	Arg	Tyr	Tyr	Met	Asp
1				5					10					15	
Gly	Ser	Val	Asn	Gly	His	Glu	Phe	Thr	Ile	Glu	Gly	Glu	Gly	Thr	Gly
				20					25					30	
Arg	Pro	Tyr	Glu	Gly	His	Gln	Glu	Met	Thr	Leu	Arg	Val	Thr	Met	Ala
				35					40					45	
Glu	Gly	Gly	Pro	Met	Pro	Phe	Ala	Phe	Asp	Leu	Val	Ser	His	Val	Phe
				50					55					60	
Cys	Tyr	Gly	His	Arg	Cys	Phe	Thr	Lys	Tyr	Pro	Glu	Glu	Ile	Pro	Asp
				65					70					75	
Tyr	Phe	Lys	Gln	Ala	Phe	Pro	Glu	Gly	Leu	Ser	Trp	Glu	Arg	Ser	Leu
				85					90					95	
Glu	Phe	Glu	Asp	Gly	Gly	Ser	Ala	Ser	Val	Ser	Ala	His	Ile	Ser	Leu
				100					105					110	
Arg	Gly	Asn	Thr	Phe	Tyr	His	Lys	Ser	Lys	Phe	Thr	Gly	Val	Asn	Phe
				115					120					125	
Pro	Ala	Asp	Gly	Pro	Ile	Met	Gln	Asn	Gln	Ser	Val	Asp	Trp	Glu	Pro
				130					135					140	
Ser	Thr	Glu	Lys	Ile	Thr	Ala	Ser	Asp	Gly	Val	Leu	Lys	Gly	Asp	Val
				145					150					155	
Thr	Met	Tyr	Leu	Lys	Leu	Glu	Gly	Gly	Gly	Asn	His	Lys	Cys	Gln	Phe
				165					170					175	
Lys	Thr	Thr	Tyr	Lys	Ala	Ala	Lys	Glu	Ile	Leu	Glu	Met	Pro	Gly	Asp
				180					185					190	
His	Tyr	Ile	Gly	His	Arg	Leu	Val	Arg	Lys	Thr	Glu	Gly	Asn	Ile	Thr

195                                      200                                      205  
 Glu Leu Val Glu Asp Ala Val Ala His Ser  
 210                                      215  
 <210> 18  
 <211> 657  
 <212> DNA  
 <213> *Fungia* sp.  
 <400> 18  
 atg gtg agt gtg att aaa cca gag atg aag atg agg tac tac atg gac 48  
 Met Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp  
 1                                      5                                      10                                      15  
 ggc tcc gtc aat ggg cat gag ttc aca att gaa ggt gaa ggc aca ggc 96  
 Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly  
 20                                      25                                      30  
 aga cct tac gag gga cat caa gag atg aca cta cgc gtc aca atg gcc 144  
 Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala  
 35                                      40                                      45  
 gag ggc ggg cca atg cct ttc gcg ttt gac tta gtg tca cac gtg ttc 192  
 Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe  
 50                                      55                                      60  
 tgt tac ggc cac aga tgt ttt act aaa tat cca gaa gag ata cca gac 240  
 Cys Tyr Gly His Arg Cys Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp  
 65                                      70                                      75                                      80  
 tat ttc aaa caa gca ttt cct gaa ggc ctg tca tgg gaa agg tcg ttg 288  
 Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu  
 85                                      90                                      95  
 gag ttc gaa gat ggt ggg tcc gct tca gtc agt gcg cat ata agc ctt 336

Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu  
 100 105 110  
 aga gga aac acc ttc tac cac aaa tcc aaa ttt act ggg gtt aac ttt 384  
 Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe  
 115 120 125  
 cct gcc gat ggt cct atc atg caa aac caa agt gtt gat tgg gag cca 432  
 Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro  
 130 135 140  
 tca acc gag aaa att act gcc agc gac gga gtt ctg aag ggt gat gtt 480  
 Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val  
 145 150 155 160  
 acg atg tac cta aaa ctt gaa gga ggc ggc aat cac aaa tgc caa ttc 528  
 Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe  
 165 170 175  
 aag act act tac aag gcg gca aaa gag att ctt gaa atg cca gga gac 576  
 Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp  
 180 185 190  
 cat tac atc ggc cat cgc ctc gtc agg aaa acc gaa ggc aac att act 624  
 His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr  
 195 200 205  
 gag ctg gta gaa gat gca gta gct cat tcc taa 657  
 Glu Leu Val Glu Asp Ala Val Ala His Ser  
 210 215

<210> 19

<211> 218

<212> PRT

<213> Fungia sp.

<400> 19

Met Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp

1 5 10 15

Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly

20 25 30

Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala

35 40 45

Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe

50 55 60

Cys Tyr Gly His Arg Thr Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp

65 70 75 80

Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu

85 90 95

Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu

100 105 110

Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe

115 120 125

Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro

130 135 140

Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val

145 150 155 160

Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe

165 170 175

Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp

180 185 190

His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr

195 200 205

Glu Leu Val Glu Asp Ala Val Ala His Ser

210

215

<210> 20

<211> 657

<212> DNA

<213> Fungia sp.

<400> 20

atg gtg agt gtg att aaa cca gag atg aag atg agg tac tac atg gac 48

Met Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp

1

5

10

15

ggc tcc gtc aat ggg cat gag ttc aca att gaa ggt gaa ggc aca ggc 96

Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly

20

25

30

aga cct tac gag gga cat caa gag atg aca cta cgc gtc aca atg gcc 144

Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala

35

40

45

gag ggc ggg cca atg cct ttc gcg ttt gac tta gtg tca cac gtg ttc 192

Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe

50

55

60

tgt tac ggc cac aga act ttt act aaa tat cca gaa gag ata cca gac 240

Cys Tyr Gly His Arg Thr Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp

65

70

75

80

tat ttc aaa caa gca ttt cct gaa ggc ctg tca tgg gaa agg tcg ttg 288

Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu

85

90

95

gag ttc gaa gat ggt ggg tcc gct tca gtc agt gcg cat ata agc ctt 336

Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu

100	105	110	
aga gga aac acc ttc tac cac aaa tcc aaa ttt act ggg gtt aac ttt 384			
Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe			
115	120	125	
cct gcc gat ggt cct atc atg caa aac caa agt gtt gat tgg gag cca 432			
Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro			
130	135	140	
tca acc gag aaa att act gcc agc gac gga gtt ctg aag ggt gat gtt 480			
Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val			
145	150	155	160
acg atg tac cta aaa ctt gaa gga ggc ggc aat cac aaa tgc caa ttc 528			
Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe			
165	170	175	
aag act act tac aag gcg gca aaa gag att ctt gaa atg cca gga gac 576			
Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp			
180	185	190	
cat tac atc ggc cat cgc ctc gtc agg aaa acc gaa ggc aac att act 624			
His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr			
195	200	205	
gag ctg gta gaa gat gca gta gct cat tcc taa			657
Glu Leu Val Glu Asp Ala Val Ala His Ser			

210                      215

<210> 21

<211> 218

<212> PRT

<213> *Fungia* sp.

<400> 21

Met Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp  
 1 5 10 15  
 Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly  
 20 25 30  
 Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala  
 35 40 45  
 Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe  
 50 55 60  
 Cys Tyr Gly His Arg Val Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp  
 65 70 75 80  
 Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu  
 85 90 95  
 Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu  
 100 105 110  
 Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe  
 115 120 125  
 Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro  
 130 135 140  
 Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val  
 145 150 155 160  
 Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe  
 165 170 175  
 Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp  
 180 185 190  
 His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr  
 195 200 205  
 Glu Leu Val Glu Asp Ala Val Ala His Ser

210

215

&lt;210&gt; 22

&lt;211&gt; 657

&lt;212&gt; DNA

&lt;213&gt; Fungia sp.

&lt;400&gt; 22

atg gtg agt gtg att aaa cca gag atg aag atg agg tac tac atg gac 48

Met Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp

1

5

10

15

ggc tcc gtc aat ggg cat gag ttc aca att gaa ggt gaa ggc aca ggc 96

Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly

20

25

30

aga cct tac gag gga cat caa gag atg aca cta cgc gtc aca atg gcc 144

Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala

35

40

45

gag ggc ggg cca atg cct ttc gcg ttt gac tta gtg tca cac gtg ttc 192

Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe

50

55

60

tgt tac ggc cac aga gta ttt act aaa tat cca gaa gag ata cca gac 240

Cys Tyr Gly His Arg Val Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp

65

70

75

80

tat ttc aaa caa gca ttt cct gaa ggc ctg tca tgg gaa agg tcg ttg 288

Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu

85

90

95

gag ttc gaa gat ggt ggg tcc gct tca gtc agt gcg cat ata agc ctt 336

Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu

100

105

110



aga gga aac acc ttc tac cac aaa tcc aaa ttt act ggg gtt aac ttt 384  
 Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe  
 115 120 125  
 cct gcc gat ggt cct atc atg caa aac caa agt gtt gat tgg gag cca 432  
 Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro  
 130 135 140  
 tca acc gag aaa att act gcc agc gac gga gtt ctg aag ggt gat gtt 480  
 Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val  
 145 150 155 160  
 acg atg tac cta aaa ctt gaa gga ggc ggc aat cac aaa tgc caa ttc 528  
 Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe  
 165 170 175  
 aag act act tac aag gcg gca aaa gag att ctt gaa atg cca gga gac 576  
 Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp  
 180 185 190  
 cat tac atc ggc cat cgc ctc gtc agg aaa acc gaa ggc aac att act 624  
 His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr  
 195 200 205  
 gag ctg gta gaa gat gca gta gct cat tcc taa 657  
 Glu Leu Val Glu Asp Ala Val Ala His Ser  
 210 215

<210> 23

<211> 218

<212> PRT

<213> *Fungia* sp.

<400> 23

Met Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp

1	5	10	15
Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly			
20	25	30	
Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala			
35	40	45	
Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe			
50	55	60	
Cys Tyr Gly His Arg Leu Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp			
65	70	75	80
Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu			
85	90	95	
Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu			
100	105	110	
Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe			
115	120	125	
Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro			
130	135	140	
Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val			
145	150	155	160
Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe			
165	170	175	
Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp			
180	185	190	
His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr			
195	200	205	
Glu Leu Val Glu Asp Ala Val Ala His Ser			
210	215		

<210> 24

<211> 657

<212> DNA

<213> Fungia sp.

<400> 24

```
atg gtg agt gtg att aaa cca gag atg aag atg agg tac tac atg gac 48
Met Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp
      1              5              10              15
ggc tcc gtc aat ggg cat gag ttc aca att gaa ggt gaa ggc aca ggc 96
Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly
              20              25              30
aga cct tac gag gga cat caa gag atg aca cta cgc gtc aca atg gcc 144
Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala
              35              40              45
gag ggc ggg cca atg cct ttc gcg ttt gac tta gtg tca cac gtg ttc 192
Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe
              50              55              60
tgt tac ggc cac aga ctt ttt act aaa tat cca gaa gag ata cca gac 240
Cys Tyr Gly His Arg Leu Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp
              65              70              75              80
tat ttc aaa caa gca ttt cct gaa ggc ctg tca tgg gaa agg tcg ttg 288
Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu
              85              90              95
gag ttc gaa gat ggt ggg tcc gct tca gtc agt gcg cat ata agc ctt 336
Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu
              100             105             110
aga gga aac acc ttc tac cac aaa tcc aaa ttt act ggg gtt aac ttt 384
```

Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe  
 115 120 125  
 cct gcc gat ggt cct atc atg caa aac caa agt gtt gat tgg gag cca 432  
 Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro  
 130 135 140  
 tca acc gag aaa att act gcc agc gac gga gtt ctg aag ggt gat gtt 480  
 Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val  
 145 150 155 160  
 acg atg tac cta aaa ctt gaa gga ggc ggc aat cac aaa tgc caa ttc 528  
 Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe  
 165 170 175  
 aag act act tac aag gcg gca aaa gag att ctt gaa atg cca gga gac 576  
 Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp  
 180 185 190  
 cat tac atc ggc cat cgc ctc gtc agg aaa acc gaa ggc aac att act 624  
 His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr  
 195 200 205  
 gag ctg gta gaa gat gca gta gct cat tcc taa 657  
 Glu Leu Val Glu Asp Ala Val Ala His Ser

210 215

<210> 25

<211> 218

<212> PRT

<213> *Fungia* sp.

<400> 25

Met Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp

1

5

10

15

Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly			
20	25	30	
Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala			
35	40	45	
Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe			
50	55	60	
Cys Tyr Gly His Arg Tyr Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp			
65	70	75	80
Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu			
85	90	95	
Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu			
100	105	110	
Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe			
115	120	125	
Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro			
130	135	140	
Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val			
145	150	155	160
Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe			
165	170	175	
Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp			
180	185	190	
His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr			
195	200	205	
Glu Leu Val Glu Asp Ala Val Ala His Ser			
210	215		

<210> 26

<211> 657

<212> DNA

<213> Fungia sp.

<400> 26

```
atg gtg agt gtg att aaa cca gag atg aag atg agg tac tac atg gac 48
Met Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp
      1              5              10              15
ggc tcc gtc aat ggg cat gag ttc aca att gaa ggt gaa ggc aca ggc 96
Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly
              20              25              30
aga cct tac gag gga cat caa gag atg aca cta cgc gtc aca atg gcc 144
Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala
              35              40              45
gag ggc ggg cca atg cct ttc gcg ttt gac tta gtg tca cac gtg ttc 192
Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe
              50              55              60
tgt tac ggc cac aga tac ttt act aaa tat cca gaa gag ata cca gac 240
Cys Tyr Gly His Arg Tyr Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp
              65              70              75              80
tat ttc aaa caa gca ttt cct gaa ggc ctg tca tgg gaa agg tcg ttg 288
Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu
              85              90              95
gag ttc gaa gat ggt ggg tcc gct tca gtc agt gcg cat ata agc ctt 336
Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu
              100             105             110
aga gga aac acc ttc tac cac aaa tcc aaa ttt act ggg gtt aac ttt 384
Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe
```

115	120	125	
cct gcc gat ggt cct atc atg caa aac caa agt gtt gat tgg gag cca	432		
Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro			
130	135	140	
tca acc gag aaa att act gcc agc gac gga gtt ctg aag ggt gat gtt	480		
Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val			
145	150	155	160
acg atg tac cta aaa ctt gaa gga ggc ggc aat cac aaa tgc caa ttc	528		
Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe			
165	170	175	
aag act act tac aag gcg gca aaa gag att ctt gaa atg cca gga gac	576		
Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp			
180	185	190	
cat tac atc ggc cat cgc ctc gtc agg aaa acc gaa ggc aac att act	624		
His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr			
195	200	205	
gag ctg gta gaa gat gca gta gct cat tcc taa	657		
Glu Leu Val Glu Asp Ala Val Ala His Ser			
210	215		
<210> 27			
<211> 218			
<212> PRT			
<213> <i>Fungia</i> sp.			
<400> 27			
Met Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp			
1	5	10	15
Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly			

	20	25	30
Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala			
35	40	45	
Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe			
50	55	60	
Cys Tyr Gly His Arg Gln Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp			
65	70	75	80
Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu			
85	90	95	
Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu			
100	105	110	
Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe			
115	120	125	
Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro			
130	135	140	
Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val			
145	150	155	160
Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe			
165	170	175	
Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp			
180	185	190	
His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr			
195	200	205	
Glu Leu Val Glu Asp Ala Val Ala His Ser			
210	215		
<210> 28			
<211> 657			



<212> DNA

<213> Fungia sp.

<400> 28

```
atg gtg agt gtg att aaa cca gag atg aag atg agg tac tac atg gac 48
Met Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp
      1              5              10              15
ggc tcc gtc aat ggg cat gag ttc aca att gaa ggt gaa ggc aca ggc 96
Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly
              20              25              30
aga cct tac gag gga cat caa gag atg aca cta cgc gtc aca atg gcc 144
Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala
              35              40              45
gag ggc ggg cca atg cct ttc gcg ttt gac tta gtg tca cac gtg ttc 192
Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe
              50              55              60
tgt tac ggc cac aga cag ttt act aaa tat cca gaa gag ata cca gac 240
Cys Tyr Gly His Arg Gln Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp
              65              70              75              80
tat ttc aaa caa gca ttt cct gaa ggc ctg tca tgg gaa agg tcg ttg 288
Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu
              85              90              95
gag ttc gaa gat ggt ggg tcc gct tca gtc agt gcg cat ata agc ctt 336
Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu
              100              105              110
aga gga aac acc ttc tac cac aaa tcc aaa ttt act ggg gtt aac ttt 384
Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe
              115              120              125
```

cct gcc gat ggt cct atc atg caa aac caa agt gtt gat tgg gag cca 432  
 Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro  
 130 135 140  
 tca acc gag aaa att act gcc agc gac gga gtt ctg aag ggt gat gtt 480  
 Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val  
 145 150 155 160  
 acg atg tac cta aaa ctt gaa gga ggc ggc aat cac aaa tgc caa ttc 528  
 Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe  
 165 170 175  
 aag act act tac aag gcg gca aaa gag att ctt gaa atg cca gga gac 576  
 Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp  
 180 185 190  
 cat tac atc ggc cat cgc ctc gtc agg aaa acc gaa ggc aac att act 624  
 His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr  
 195 200 205  
 gag ctg gta gaa gat gca gta gct cat tcc taa 657  
 Glu Leu Val Glu Asp Ala Val Ala His Ser  
 210 215

<210> 29

<211> 218

<212> PRT

<213> *Fungia* sp.

<220>

<221> UNSURE

<222> (186)

<223> unknown amino acid

<400> 29

Met	Val	Ser	Val	Ile	Lys	Pro	Glu	Met	Lys	Met	Arg	Tyr	Tyr	Met	Asp
1				5					10					15	
Gly	Ser	Val	Asn	Gly	His	Glu	Phe	Thr	Ile	Glu	Gly	Glu	Gly	Thr	Gly
			20					25					30		
Arg	Pro	Tyr	Glu	Gly	His	Gln	Glu	Met	Thr	Leu	Arg	Val	Thr	Met	Ala
		35				40					45				
Glu	Gly	Gly	Pro	Met	Pro	Phe	Ala	Phe	Asp	Leu	Val	Ser	His	Val	Phe
	50					55					60				
Cys	Tyr	Gly	His	Arg	Asn	Phe	Thr	Lys	Tyr	Pro	Glu	Glu	Ile	Pro	Asp
65				70					75					80	
Tyr	Phe	Lys	Gln	Ala	Phe	Pro	Glu	Gly	Leu	Ser	Trp	Glu	Arg	Ser	Leu
			85					90					95		
Glu	Phe	Glu	Asp	Gly	Gly	Ser	Ala	Ser	Val	Ser	Ala	His	Ile	Ser	Leu
		100					105					110			
Arg	Gly	Asn	Thr	Phe	Tyr	His	Lys	Ser	Lys	Phe	Thr	Gly	Val	Asn	Phe
	115						120					125			
Pro	Ala	Asp	Gly	Pro	Ile	Met	Gln	Asn	Gln	Ser	Val	Asp	Trp	Glu	Pro
	130					135					140				
Ser	Thr	Glu	Lys	Ile	Thr	Ala	Ser	Asp	Gly	Val	Leu	Lys	Gly	Asp	Val
145				150					155					160	
Thr	Met	Tyr	Leu	Lys	Leu	Glu	Gly	Gly	Gly	Asn	His	Lys	Cys	Gln	Phe
			165					170					175		
Lys	Thr	Thr	Tyr	Lys	Ala	Ala	Lys	Glu	Xaa	Leu	Glu	Met	Pro	Gly	Asp
		180						185					190		
His	Tyr	Ile	Gly	His	Arg	Leu	Val	Arg	Lys	Thr	Glu	Gly	Asn	Ile	Thr
	195					200					205				
Glu	Leu	Val	Glu	Asp	Ala	Val	Ala	His	Ser						

210

215

&lt;210&gt; 30

&lt;211&gt; 657

&lt;212&gt; DNA

&lt;213&gt; Fungia sp.

&lt;220&gt;

&lt;221&gt; unsure

&lt;222&gt; (556)

&lt;223&gt; unknown nucleotide

&lt;400&gt; 30

atg gtg agt gtg att aaa cca gag atg aag atg agg tac tac atg gac 48

Met Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp

1

5

10

15

ggc tcc gtc aat ggg cat gag ttc aca att gaa ggt gaa ggc aca ggc 96

Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly

20

25

30

aga cct tac gag gga cat caa gag atg aca cta cgc gtc aca atg gcc 144

Arg Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala

35

40

45

gag ggc ggg cca atg cct ttc gcg ttt gac tta gtg tca cac gtg ttc 192

Glu Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe

50

55

60

tgt tac ggc cac aga aat ttt act aaa tat cca gaa gag ata cca gac 240

Cys Tyr Gly His Arg Asn Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp

65

70

75

80

tat ttc aaa caa gca ttt cct gaa ggc ctg tca tgg gaa agg tcg ttg 288

Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu

85	90	95	
gag ttc gaa gat ggt ggg tcc gct tca gtc agt gcg cat ata agc ctt 336			
Glu Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu			
100	105	110	
aga gga aac acc ttc tac cac aaa tcc aaa ttt act ggg gtt aac ttt 384			
Arg Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe			
115	120	125	
cct gcc gat ggt cct atc atg caa aac caa agt gtt gat tgg gag cca 432			
Pro Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro			
130	135	140	
tca acc gag aaa att act gcc agc gac gga gtt ctg aag ggt gat gtt 480			
Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val			
145	150	155	160
acg atg tac cta aaa ctt gaa gga ggc ggc aat cac aaa tgc caa ttc 528			
Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe			
165	170	175	
aag act act tac aag gcg gca aaa gag ntt ctt gaa atg cca gga gac 576			
Lys Thr Thr Tyr Lys Ala Ala Lys Glu Xaa Leu Glu Met Pro Gly Asp			
180	185	190	
cat tac atc ggc cat cgc ctc gtc agg aaa acc gaa ggc aac att act 624			
His Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr			
195	200	205	
gag ctg gta gaa gat gca gta gct cat tcc taa 657			
Glu Leu Val Glu Asp Ala Val Ala His Ser			
210	215		
<210> 31			
<211> 665			

<212> PRT

<213> Fungia sp.

<400> 31

Met	Ala	Glu	Pro	Arg	Gln	Glu	Phe	Glu	Val	Met	Glu	Asp	His	Ala	Gly
1				5					10					15	
Thr	Tyr	Gly	Leu	Gly	Asp	Arg	Lys	Asp	Gln	Gly	Gly	Tyr	Thr	Met	His
			20					25					30		
Gln	Asp	Gln	Glu	Gly	Asp	Thr	Asp	Ala	Gly	Leu	Lys	Glu	Ser	Pro	Leu
		35					40					45			
Gln	Thr	Pro	Thr	Glu	Asp	Gly	Ser	Glu	Glu	Pro	Gly	Ser	Glu	Thr	Ser
	50					55					60				
Asp	Ala	Lys	Ser	Thr	Pro	Thr	Ala	Glu	Asp	Val	Thr	Ala	Pro	Leu	Val
65				70						75				80	
Asp	Glu	Gly	Ala	Pro	Gly	Lys	Gln	Ala	Ala	Ala	Gln	Pro	His	Thr	Glu
				85					90					95	
Ile	Pro	Glu	Gly	Thr	Thr	Ala	Glu	Glu	Ala	Gly	Ile	Gly	Asp	Thr	Pro
			100						105					110	
Ser	Leu	Glu	Asp	Glu	Ala	Ala	Gly	His	Val	Thr	Gln	Ala	Arg	Met	Val
			115						120					125	
Ser	Lys	Ser	Lys	Asp	Gly	Thr	Gly	Ser	Asp	Asp	Lys	Lys	Ala	Lys	Gly
	130						135						140		
Ala	Asp	Gly	Lys	Thr	Lys	Ile	Ala	Thr	Pro	Arg	Gly	Ala	Ala	Pro	Pro
145					150					155				160	
Gly	Gln	Lys	Gly	Gln	Ala	Asn	Ala	Thr	Arg	Ile	Pro	Ala	Lys	Thr	Pro
				165					170					175	
Pro	Ala	Pro	Lys	Thr	Pro	Pro	Ser	Ser	Gly	Glu	Pro	Pro	Lys	Ser	Gly
			180						185					190	

Asp Arg Ser Gly Tyr Ser Ser Pro Gly Ser Pro Gly Thr Pro Gly Ser  
 195 200 205  
 Arg Ser Arg Thr Pro Ser Leu Pro Thr Pro Pro Thr Arg Glu Pro Lys  
 210 215 220  
 Lys Val Ala Val Val Arg Thr Pro Pro Lys Ser Pro Ser Ser Ala Lys  
 225 230 235 240  
 Ser Arg Leu Gln Thr Ala Pro Val Pro Met Pro Asp Leu Lys Asn Val  
 245 250 255  
 Lys Ser Lys Ile Gly Ser Thr Glu Asn Leu Lys His Gln Pro Gly Gly  
 260 265 270  
 Gly Lys Val Gln Ile Ile Asn Lys Lys Leu Asp Leu Ser Asn Val Gln  
 275 280 285  
 Ser Lys Cys Gly Ser Lys Asp Asn Ile Lys His Val Pro Gly Gly Gly  
 290 295 300  
 Ser Val Gln Ile Val Tyr Lys Pro Val Asp Leu Ser Lys Val Thr Ser  
 305 310 315 320  
 Lys Cys Gly Ser Leu Gly Asn Ile His His Lys Pro Gly Gly Gly Gln  
 325 330 335  
 Val Glu Val Lys Ser Glu Lys Leu Asp Phe Lys Asp Arg Val Gln Ser  
 340 345 350  
 Lys Ile Gly Ser Leu Asp Asn Ile Thr His Val Pro Gly Gly Gly Asn  
 355 360 365  
 Lys Lys Ile Glu Thr His Lys Leu Thr Phe Arg Glu Asn Ala Lys Ala  
 370 375 380  
 Lys Thr Asp His Gly Ala Glu Ile Val Tyr Lys Ser Pro Val Val Ser  
 385 390 395 400  
 Gly Asp Thr Ser Pro Arg His Leu Ser Asn Val Ser Ser Thr Gly Ser

405	410	415
Ile Asp Met Val Asp Ser Pro Gln Leu Ala Thr Leu Ala Asp Glu Val		
420	425	430
Ser Ala Ser Leu Ala Lys Gln Gly Leu Gly Ser Gly Gly Glu Phe Met		
435	440	445
Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp Gly		
450	455	460
Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly Arg		
465	470	475
Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala Glu		
485	490	495
Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe Cys		
500	505	510
Tyr Gly His Arg Val Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp Tyr		
515	520	525
Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu Glu		
530	535	540
Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu Arg		
545	550	555
Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe Pro		
565	570	575
Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro Ser		
580	585	590
Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val Thr		
595	600	605
Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe Lys		
610	615	620



Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp His

625 630 635 640

Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr Glu

645 650 655

Leu Val Glu Asp Ala Val Ala His Ser

660 665

<210> 32

<211> 1998

<212> DNA

<213> Fungia sp.

<400> 32

atg gct gag ccc cgc cag gag ttc gaa gtg atg gaa gat cac gct ggg 48

Met Ala Glu Pro Arg Gln Glu Phe Glu Val Met Glu Asp His Ala Gly

1 5 10 15

acg tac ggg ttg ggg gac agg aaa gat cag ggg ggc tac acc atg cac 96

Thr Tyr Gly Leu Gly Asp Arg Lys Asp Gln Gly Gly Tyr Thr Met His

20 25 30

caa gac caa gag ggt gac acg gac gct ggc ctg aaa gaa tct ccc ctg 144

Gln Asp Gln Glu Gly Asp Thr Asp Ala Gly Leu Lys Glu Ser Pro Leu

35 40 45

cag acc ccc act gag gac gga tct gag gaa ccg ggc tct gaa acc tct 192

Gln Thr Pro Thr Glu Asp Gly Ser Glu Glu Pro Gly Ser Glu Thr Ser

50 55 60

gat gct aag agc act cca aca gcg gaa gat gtg aca gca ccc tta gtg 240

Asp Ala Lys Ser Thr Pro Thr Ala Glu Asp Val Thr Ala Pro Leu Val

65 70 75 80

gat gag gga gct ccc ggc aag cag gct gcc gcg cag ccc cac acg gag 288

Asp Glu Gly Ala Pro Gly Lys Gln Ala Ala Ala Gln Pro His Thr Glu  
                     85                    90                    95  
 atc cca gaa gga acc aca gct gaa gaa gca ggc att gga gac acc ccc 336  
 Ile Pro Glu Gly Thr Thr Ala Glu Glu Ala Gly Ile Gly Asp Thr Pro  
                     100                    105                    110  
 agc ctg gaa gac gaa gct gct ggt cac gtg acc caa gct cgc atg gtc 384  
 Ser Leu Glu Asp Glu Ala Ala Gly His Val Thr Gln Ala Arg Met Val  
                     115                    120                    125  
 agt aaa agc aaa gac ggg act gga agc gat gac aaa aaa gcc aag ggg 432  
 Ser Lys Ser Lys Asp Gly Thr Gly Ser Asp Asp Lys Lys Ala Lys Gly  
                     130                    135                    140  
 gct gat ggt aaa acg aag atc gcc aca ccg cgg gga gca gcc cct cca 480  
 Ala Asp Gly Lys Thr Lys Ile Ala Thr Pro Arg Gly Ala Ala Pro Pro  
                     145                    150                    155                    160  
 ggc cag aag ggc cag gcc aac gcc acc agg att cca gca aaa acc ccg 528  
 Gly Gln Lys Gly Gln Ala Asn Ala Thr Arg Ile Pro Ala Lys Thr Pro  
                     165                    170                    175  
 ccc gct cca aag aca cca ccc agc tct ggt gaa cct cca aaa tca ggg 576  
 Pro Ala Pro Lys Thr Pro Pro Ser Ser Gly Glu Pro Pro Lys Ser Gly  
                     180                    185                    190  
 gat cgc agc ggc tac agc agc ccc ggc tcc cca ggc act ccc ggc agc 624  
 Asp Arg Ser Gly Tyr Ser Ser Pro Gly Ser Pro Gly Thr Pro Gly Ser  
                     195                    200                    205  
 cgc tcc cgc acc ccg tcc ctt cca acc cca ccc acc cgg gag ccc aag 672  
 Arg Ser Arg Thr Pro Ser Leu Pro Thr Pro Pro Thr Arg Glu Pro Lys  
                     210                    215                    220  
 aag gtg gca gtg gtc cgt act cca ccc aag tcg ccg tct tcc gcc aag 720

Lys Val Ala Val Val Arg Thr Pro Pro Lys Ser Pro Ser Ser Ala Lys  
 225                      230                      235                      240  
 agc cgc ctg cag aca gcc ccc gtg ccc atg cca gac ctg aag aat gtc 768  
 Ser Arg Leu Gln Thr Ala Pro Val Pro Met Pro Asp Leu Lys Asn Val  
                          245                      250                      255  
 aag tcc aag atc ggc tcc act gag aac ctg aag cac cag ccg gga ggc 816  
 Lys Ser Lys Ile Gly Ser Thr Glu Asn Leu Lys His Gln Pro Gly Gly  
                          260                      265                      270  
 ggg aag gtg cag ata att aat aag aag ctg gat ctt agc aac gtc cag 864  
 Gly Lys Val Gln Ile Ile Asn Lys Lys Leu Asp Leu Ser Asn Val Gln  
                          275                      280                      285  
 tcc aag tgt ggc tca aag gat aat atc aaa cac gtc ccg gga ggc ggc 912  
 Ser Lys Cys Gly Ser Lys Asp Asn Ile Lys His Val Pro Gly Gly Gly  
                          290                      295                      300  
 agt gtg caa ata gtc tac aaa cca gtt gac ctg agc aag gtg acc tcc 960  
 Ser Val Gln Ile Val Tyr Lys Pro Val Asp Leu Ser Lys Val Thr Ser  
 305                      310                      315                      320  
 aag tgt ggc tca tta ggc aac atc cat cat aaa cca gga ggt ggc cag 1008  
 Lys Cys Gly Ser Leu Gly Asn Ile His His Lys Pro Gly Gly Gly Gln  
                          325                      330                      335  
 gtg gaa gta aaa tct gag aag ctt gac ttc aag gac aga gtc cag tcg 1056  
 Val Glu Val Lys Ser Glu Lys Leu Asp Phe Lys Asp Arg Val Gln Ser  
                          340                      345                      350  
 aag att ggg tcc ctg gac aat atc acc cac gtc cct ggc gga gga aat 1104  
 Lys Ile Gly Ser Leu Asp Asn Ile Thr His Val Pro Gly Gly Gly Asn  
                          355                      360                      365  
 aaa aag att gaa acc cac aag ctg acc ttc cgc gag aac gcc aaa gcc 1152

Lys Lys Ile Glu Thr His Lys Leu Thr Phe Arg Glu Asn Ala Lys Ala  
 370 375 380  
 aag aca gac cac ggg gcg gag atc gtg tac aag tcg cca gtg gtg tct 1200  
 Lys Thr Asp His Gly Ala Glu Ile Val Tyr Lys Ser Pro Val Val Ser  
 385 390 395 400  
 ggg gac acg tct cca cgg cat ctc agc aat gtc tcc tcc acc ggc agc 1248  
 Gly Asp Thr Ser Pro Arg His Leu Ser Asn Val Ser Ser Thr Gly Ser  
 405 410 415  
 atc gac atg gta gac tcg ccc cag ctc gcc acg cta gct gac gag gtg 1296  
 Ile Asp Met Val Asp Ser Pro Gln Leu Ala Thr Leu Ala Asp Glu Val  
 420 425 430  
 tct gcc tcc ctg gcc aag cag ggt ttg gga tcc gga ggt gaa ttc atg 1344  
 Ser Ala Ser Leu Ala Lys Gln Gly Leu Gly Ser Gly Gly Glu Phe Met  
 435 440 445  
 gtg agt gtg att aaa cca gag atg aag atg agg tac tac atg gac ggc 1392  
 Val Ser Val Ile Lys Pro Glu Met Lys Met Arg Tyr Tyr Met Asp Gly  
 450 455 460  
 tcc gtc aat ggg cat gag ttc aca att gaa ggt gaa ggc aca ggc aga 1440  
 Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly Glu Gly Thr Gly Arg  
 465 470 475 480  
 cct tac gag gga cat caa gag atg aca cta cgc gtc aca atg gcc gag 1488  
 Pro Tyr Glu Gly His Gln Glu Met Thr Leu Arg Val Thr Met Ala Glu  
 485 490 495  
 ggc ggg cca atg cct ttc gcg ttt gac tta gtg tca cac gtg ttc tgt 1536  
 Gly Gly Pro Met Pro Phe Ala Phe Asp Leu Val Ser His Val Phe Cys  
 500 505 510  
 tac ggc cac aga gta ttt act aaa tat cca gaa gag ata cca gac tat 1584

Tyr Gly His Arg Val Phe Thr Lys Tyr Pro Glu Glu Ile Pro Asp Tyr  
515 520 525  
ttc aaa caa gca ttt cct gaa ggc ctg tca tgg gaa agg tcg ttg gag 1632  
Phe Lys Gln Ala Phe Pro Glu Gly Leu Ser Trp Glu Arg Ser Leu Glu  
530 535 540  
ttc gaa gat ggt ggg tcc gct tca gtc agt gcg cat ata agc ctt aga 1680  
Phe Glu Asp Gly Gly Ser Ala Ser Val Ser Ala His Ile Ser Leu Arg  
545 550 555 560  
gga aac acc ttc tac cac aaa tcc aaa ttt act ggg gtt aac ttt cct 1728  
Gly Asn Thr Phe Tyr His Lys Ser Lys Phe Thr Gly Val Asn Phe Pro  
565 570 575  
gcc gat ggt cct atc atg caa aac caa agt gtt gat tgg gag cca tca 1776  
Ala Asp Gly Pro Ile Met Gln Asn Gln Ser Val Asp Trp Glu Pro Ser  
580 585 590  
acc gag aaa att act gcc agc gac gga gtt ctg aag ggt gat gtt acg 1824  
Thr Glu Lys Ile Thr Ala Ser Asp Gly Val Leu Lys Gly Asp Val Thr  
595 600 605  
atg tac cta aaa ctt gaa gga ggc ggc aat cac aaa tgc caa ttc aag 1872  
Met Tyr Leu Lys Leu Glu Gly Gly Gly Asn His Lys Cys Gln Phe Lys  
610 615 620  
act act tac aag gcg gca aaa gag att ctt gaa atg cca gga gac cat 1920  
Thr Thr Tyr Lys Ala Ala Lys Glu Ile Leu Glu Met Pro Gly Asp His  
625 630 635 640  
tac atc ggc cat cgc ctc gtc agg aaa acc gaa ggc aac att act gag 1968  
Tyr Ile Gly His Arg Leu Val Arg Lys Thr Glu Gly Asn Ile Thr Glu  
645 650 655  
ctg gta gaa gat gca gta gct cat tcc taa 1998

Leu Val Glu Asp Ala Val Ala His Ser

660

665

<210> 33

<211> 480

<212> PRT

<213> Fungia sp.

<400> 33

Met Gly Thr Ile Leu Phe Leu Thr Met Val Ile Ser Tyr Phe Gly Cys

1

5

10

15

Met Lys Ala Ala Pro Met Lys Glu Ala Asn Val His Gly Gln Gly Asn

20

25

30

Leu Ala Tyr Pro Ala Val Arg Thr His Gly Thr Leu Glu Ser Val Asn

35

40

45

Gly Pro Arg Ala Gly Ser Arg Gly Leu Thr Thr Thr Ser Leu Ala Asp

50

55

60

Thr Phe Glu His Val Ile Glu Glu Leu Leu Asp Glu Asp Gln Lys Val

65

70

75

80

Arg Pro Asn Glu Glu Asn His Lys Asp Ala Asp Leu Tyr Thr Ser Arg

85

90

95

Val Met Leu Ser Ser Gln Val Pro Leu Glu Pro Pro Leu Leu Phe Leu

100

105

110

Leu Glu Glu Tyr Lys Asn Tyr Leu Asp Ala Ala Asn Met Ser Met Arg

115

120

125

Val Arg Arg His Ser Asp Pro Ala Arg Arg Gly Glu Leu Ser Val Cys

130

135

140

Asp Ser Ile Ser Glu Trp Val Thr Ala Ala Asp Lys Lys Thr Ala Val

145

150

155

160

Asp Met Ser Gly Gly Thr Val Thr Val Leu Glu Lys Val Pro Val Ser			
	165	170	175
Lys Gly Gln Leu Lys Gln Tyr Phe Tyr Glu Thr Lys Cys Asn Pro Met			
	180	185	190
Gly Tyr Thr Lys Glu Gly Cys Arg Gly Ile Asp Lys Arg His Trp Asn			
	195	200	205
Ser Gln Cys Arg Thr Thr Gln Ser Tyr Val Arg Ala Leu Thr Met Asp			
	210	215	220
Ser Lys Lys Arg Ile Gly Trp Arg Phe Ile Arg Ile Asp Thr Ser Cys			
225	230	235	240
Val Cys Thr Leu Thr Ile Lys Arg Gly Arg Gly Val Pro Arg Ala Arg			
	245	250	255
Asp Pro Pro Val Ala Thr Met Val Ser Val Ile Lys Pro Glu Met Lys			
	260	265	270
Met Arg Tyr Tyr Met Asp Gly Ser Val Asn Gly His Glu Phe Thr Ile			
	275	280	285
Glu Gly Glu Gly Thr Gly Arg Pro Tyr Glu Gly His Gln Glu Met Thr			
	290	295	300
Leu Arg Val Thr Met Ala Glu Gly Gly Pro Met Pro Phe Ala Phe Asp			
305	310	315	320
Leu Val Ser His Val Phe Cys Tyr Gly His Arg Val Phe Thr Lys Tyr			
	325	330	335
Pro Glu Glu Ile Pro Asp Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu			
	340	345	350
Ser Trp Glu Arg Ser Leu Glu Phe Glu Asp Gly Gly Ser Ala Ser Val			
	355	360	365
Ser Ala His Ile Ser Leu Arg Gly Asn Thr Phe Tyr His Lys Ser Lys			

370	375	380	
Phe Thr Gly Val Asn Phe Pro Ala Asp Gly Pro Ile Met Gln Asn Gln			
385	390	395	400
Ser Val Asp Trp Glu Pro Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly			
405	410	415	
Val Leu Lys Gly Asp Val Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly			
420	425	430	
Asn His Lys Cys Gln Phe Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile			
435	440	445	
Leu Glu Met Pro Gly Asp His Tyr Ile Gly His Arg Leu Val Arg Lys			
450	455	460	
Thr Glu Gly Asn Ile Thr Glu Leu Val Glu Asp Ala Val Ala His Ser			
465	470	475	480

<210> 34

<211> 1443

<212> DNA

<213> Fungia sp.

<400> 34

atg gga acc atc ctt ttc ctt act atg gtt att tca tac ttc ggt tgc 48

Met Gly Thr Ile Leu Phe Leu Thr Met Val Ile Ser Tyr Phe Gly Cys

1	5	10	15
---	---	----	----

atg aag gct gcg ccc atg aaa gaa gca aac gtc cac gga caa ggc aac 96

Met Lys Ala Ala Pro Met Lys Glu Ala Asn Val His Gly Gln Gly Asn

20	25	30
----	----	----

ttg gcc tac cca gct gtg cgg acc cat ggg act ctg gag agc gtg aat 144

Leu Ala Tyr Pro Ala Val Arg Thr His Gly Thr Leu Glu Ser Val Asn

35	40	45
----	----	----



ggg ccc agg gca ggt tcg aga ggt ctg acg acg acg tcc ctg gct gac 192  
 Gly Pro Arg Ala Gly Ser Arg Gly Leu Thr Thr Thr Ser Leu Ala Asp  
 50 55 60  
 act ttt gag cac gtg atc gaa gag ctg ctg gat gag gac cag aag gtt 240  
 Thr Phe Glu His Val Ile Glu Glu Leu Leu Asp Glu Asp Gln Lys Val  
 65 70 75 80  
 cgg ccc aac gaa gaa aac cat aag gac gcg gac ttg tac act tcc cgg 288  
 Arg Pro Asn Glu Glu Asn His Lys Asp Ala Asp Leu Tyr Thr Ser Arg  
 85 90 95  
 gtg atg ctc agc agt caa gtg cct ttg gag cct cct ctg ctc ttt ctg 336  
 Val Met Leu Ser Ser Gln Val Pro Leu Glu Pro Pro Leu Leu Phe Leu  
 100 105 110  
 ctg gag gaa tac aaa aat tac ctg gat gcc gca aac atg tct atg agg 384  
 Leu Glu Glu Tyr Lys Asn Tyr Leu Asp Ala Ala Asn Met Ser Met Arg  
 115 120 125  
 gtt cgg cgc cac tcc gac ccc gcc cgc cgt ggg gag ctg agc gtg tgt 432  
 Val Arg Arg His Ser Asp Pro Ala Arg Arg Gly Glu Leu Ser Val Cys  
 130 135 140  
 gac agt att agc gag tgg gtc aca gcg gca gat aaa aag act gca gtg 480  
 Asp Ser Ile Ser Glu Trp Val Thr Ala Ala Asp Lys Lys Thr Ala Val  
 145 150 155 160  
 gac atg tcc ggt ggg acg gtc aca gtc ctg gag aaa gtc ccg gta tca 528  
 Asp Met Ser Gly Gly Thr Val Thr Val Leu Glu Lys Val Pro Val Ser  
 165 170 175  
 aaa ggc caa ctg aag caa tat ttc tac gag acc aag tgt aat ccc atg 576  
 Lys Gly Gln Leu Lys Gln Tyr Phe Tyr Glu Thr Lys Cys Asn Pro Met  
 180 185 190

ggt tac acg aag gaa ggc tgc agg ggc ata gac aaa agg cac tgg aac 624  
 Gly Tyr Thr Lys Glu Gly Cys Arg Gly Ile Asp Lys Arg His Trp Asn  
 195 200 205  
 tcg caa tgc cga act acc caa tcg tat gtt cgg gcc ctt act atg gat 672  
 Ser Gln Cys Arg Thr Thr Gln Ser Tyr Val Arg Ala Leu Thr Met Asp  
 210 215 220  
 agc aaa aag aga att ggc tgg cgg ttc ata agg ata gac act tcc tgt 720  
 Ser Lys Lys Arg Ile Gly Trp Arg Phe Ile Arg Ile Asp Thr Ser Cys  
 225 230 235 240  
 gta tgt aca ctg acc att aaa agg gga aga ggg gta ccg cgg gcc cgg 768  
 Val Cys Thr Leu Thr Ile Lys Arg Gly Arg Gly Val Pro Arg Ala Arg  
 245 250 255  
 gac cca ccg gtc gcc acc atg gtg agt gtg att aaa cca gag atg aag 816  
 Asp Pro Pro Val Ala Thr Met Val Ser Val Ile Lys Pro Glu Met Lys  
 260 265 270  
 atg agg tac tac atg gac ggc tcc gtc aat ggg cat gag ttc aca att 864  
 Met Arg Tyr Tyr Met Asp Gly Ser Val Asn Gly His Glu Phe Thr Ile  
 275 280 285  
 gaa ggt gaa ggc aca ggc aga cct tac gag gga cat caa gag atg aca 912  
 Glu Gly Glu Gly Thr Gly Arg Pro Tyr Glu Gly His Gln Glu Met Thr  
 290 295 300  
 cta cgc gtc aca atg gcc gag ggc ggg cca atg cct ttc gcg ttt gac 960  
 Leu Arg Val Thr Met Ala Glu Gly Gly Pro Met Pro Phe Ala Phe Asp  
 305 310 315 320  
 tta gtg tca cac gtg ttc tgt tac ggc cac aga gta ttt act aaa tat 1008  
 Leu Val Ser His Val Phe Cys Tyr Gly His Arg Val Phe Thr Lys Tyr  
 325 330 335

cca gaa gag ata cca gac tat ttc aaa caa gca ttt cct gaa ggc ctg 1056  
Pro Glu Glu Ile Pro Asp Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu  
340 345 350

tca tgg gaa agg tcg ttg gag ttc gaa gat ggt ggg tcc gct tca gtc 1104  
Ser Trp Glu Arg Ser Leu Glu Phe Glu Asp Gly Gly Ser Ala Ser Val  
355 360 365

agt gcg cat ata agc ctt aga gga aac acc ttc tac cac aaa tcc aaa 1152  
Ser Ala His Ile Ser Leu Arg Gly Asn Thr Phe Tyr His Lys Ser Lys  
370 375 380

ttt act ggg gtt aac ttt cct gcc gat ggt cct atc atg caa aac caa 1200  
Phe Thr Gly Val Asn Phe Pro Ala Asp Gly Pro Ile Met Gln Asn Gln  
385 390 395 400

agt gtt gat tgg gag cca tca acc gag aaa att act gcc agc gac gga 1248  
Ser Val Asp Trp Glu Pro Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly  
405 410 415

gtt ctg aag ggt gat gtt acg atg tac cta aaa ctt gaa gga ggc ggc 1296  
Val Leu Lys Gly Asp Val Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly  
420 425 430

aat cac aaa tgc caa ttc aag act act tac aag gcg gca aaa gag att 1344  
Asn His Lys Cys Gln Phe Lys Thr Thr Tyr Lys Ala Ala Lys Glu Ile  
435 440 445

ctt gaa atg cca gga gac cat tac atc ggc cat cgc ctc gtc agg aaa 1392  
Leu Glu Met Pro Gly Asp His Tyr Ile Gly His Arg Leu Val Arg Lys  
450 455 460

acc gaa ggc aac att act gag ctg gta gaa gat gca gta gct cat tcc 1440  
Thr Glu Gly Asn Ile Thr Glu Leu Val Glu Asp Ala Val Ala His Ser  
465 470 475 480

taa

1443

<210> 35

<211> 464

<212> PRT

<213> *Fungia* sp.

<400> 35

Met Val Ser Tyr Ser Lys Gln Gly Ile Ala Gln Glu Met Arg Thr Lys

1

5

10

15

Tyr Arg Met Glu Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly

20

25

30

Val Gly Thr Gly Asn Pro Tyr Glu Gly Lys Gln Met Ser Glu Leu Val

35

40

45

Ile Ile Lys Ser Lys Gly Lys Pro Leu Pro Phe Ser Phe Asp Ile Leu

50

55

60

Ser Thr Ala Phe Gln Tyr Gly Asn Arg Cys Phe Thr Lys Tyr Pro Ala

65

70

75

80

Asp Met Pro Asp Tyr Phe Lys Gln Ala Phe Pro Asp Gly Met Ser Tyr

85

90

95

Glu Arg Ser Phe Leu Phe Glu Asp Gly Gly Val Ala Thr Ala Ser Trp

100

105

110

Ser Ile Arg Leu Glu Gly Asn Cys Phe Ile His Asn Ser Ile Tyr His

115

120

125

Gly Val Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Gln Thr Ile

130

135

140

Gly Trp Asp Lys Ser Phe Glu Lys Met Ser Val Ala Lys Glu Val Leu

145

150

155

160

Arg Gly Asp Val Thr Gln Phe Leu Leu Leu Glu Gly Gly Gly Tyr Gln

	165	170	175
Arg Cys Arg Phe His Ser Thr Tyr Lys Thr Glu Lys Pro Val Ala Met			
	180	185	190
Pro Pro Ser His Val Val Glu His Gln Ile Val Arg Thr Asp Leu Gly			
	195	200	205
Gln Thr Ala Lys Gly Phe Lys Val Lys Leu Glu Glu His Ala Glu Ala			
	210	215	220
His Val Asn Pro Leu Lys Val Lys Gly Gly Ser Gly Gly Asp Glu Val			
225	230	235	240
Asp Gly Thr Gly Gly Ser Met Val Ser Val Ile Lys Pro Glu Met Lys			
	245	250	255
Met Arg Tyr Tyr Met Asp Gly Ser Val Asn Gly His Glu Phe Thr Ile			
	260	265	270
Glu Gly Glu Gly Thr Gly Arg Pro Tyr Glu Gly His Gln Glu Met Thr			
	275	280	285
Leu Arg Val Thr Met Ala Lys Gly Gly Pro Met Pro Phe Ala Phe Asp			
	290	295	300
Leu Val Ser His Val Phe Cys Tyr Gly His Arg Pro Phe Thr Lys Tyr			
305	310	315	320
Pro Glu Glu Ile Pro Asp Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu			
	325	330	335
Ser Trp Glu Arg Ser Leu Glu Phe Glu Asp Gly Gly Ser Ala Ser Val			
	340	345	350
Ser Ala His Ile Ser Leu Arg Gly Asn Thr Phe Tyr His Lys Ser Lys			
	355	360	365
Phe Thr Gly Val Asn Phe Pro Ala Asp Gly Pro Ile Met Gln Asn Gln			
	370	375	380

Ser Val Asp Trp Glu Pro Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly  
385 390 395 400  
Val Leu Lys Gly Asp Val Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly  
405 410 415  
Asn His Lys Cys Gln Phe Lys Thr Thr Tyr Lys Ala Ala Lys Lys Ile  
420 425 430  
Leu Lys Met Pro Gly Ser His Tyr Ile Ser His Arg Leu Val Arg Lys  
435 440 445  
Thr Glu Gly Asn Ile Thr Glu Leu Val Glu Asp Ala Val Ala His Ser  
450 455 460

<210> 36

<211> 1395

<212> DNA

<213> *Fungia* sp.

<400> 36

atg gtg tct tat tca aag caa ggc atc gca caa gaa atg cgg acg aaa 48  
Met Val Ser Tyr Ser Lys Gln Gly Ile Ala Gln Glu Met Arg Thr Lys  
1 5 10 15  
tac cgt atg gaa ggc agt gtc aat ggc cat gaa ttc acg atc gaa ggt 96  
Tyr Arg Met Glu Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly  
20 25 30  
gta gga act gga aac cct tac gaa ggg aaa cag atg tcc gaa tta gtg 144  
Val Gly Thr Gly Asn Pro Tyr Glu Gly Lys Gln Met Ser Glu Leu Val  
35 40 45  
atc atc aag tct aag gga aaa ccc ctt cca ttc tcc ttt gac ata ctg 192  
Ile Ile Lys Ser Lys Gly Lys Pro Leu Pro Phe Ser Phe Asp Ile Leu  
50 55 60

tca aca gcc ttt caa tat gga aac aga tgc ttc aca aag tac cct gca 240  
Ser Thr Ala Phe Gln Tyr Gly Asn Arg Cys Phe Thr Lys Tyr Pro Ala  
65 70 75 80  
gac atg cct gac tat ttc aag caa gca ttc cca gat gga atg tca tat 288  
Asp Met Pro Asp Tyr Phe Lys Gln Ala Phe Pro Asp Gly Met Ser Tyr  
85 90 95  
gaa agg tca ttt cta ttt gag gat gga gga gtt gct aca gcc agc tgg 336  
Glu Arg Ser Phe Leu Phe Glu Asp Gly Gly Val Ala Thr Ala Ser Trp  
100 105 110  
agc att cgt ctc gaa gga aat tgc ttc atc cac aat tcc atc tat cat 384  
Ser Ile Arg Leu Glu Gly Asn Cys Phe Ile His Asn Ser Ile Tyr His  
115 120 125  
ggc gta aac ttt ccc gct gat gga ccc gta atg aag aag cag aca att 432  
Gly Val Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Gln Thr Ile  
130 135 140  
ggc tgg gat aag tcc ttc gaa aaa atg agt gtg gct aaa gag gtg cta 480  
Gly Trp Asp Lys Ser Phe Glu Lys Met Ser Val Ala Lys Glu Val Leu  
145 150 155 160  
aga ggt gat gtg act cag ttt ctt ctg ctc gaa gga ggt ggt tac cag 528  
Arg Gly Asp Val Thr Gln Phe Leu Leu Leu Glu Gly Gly Gly Tyr Gln  
165 170 175  
aga tgc cgg ttt cac tcc act tac aaa acg gag aag cca gtc gca atg 576  
Arg Cys Arg Phe His Ser Thr Tyr Lys Thr Glu Lys Pro Val Ala Met  
180 185 190  
ccc ccg agt cat gtc gta gaa cat caa att gtg agg acc gac ctt ggc 624  
Pro Pro Ser His Val Val Glu His Gln Ile Val Arg Thr Asp Leu Gly  
195 200 205

caa act gca aaa ggc ttc aag gtc aag ctg gaa gaa cat gct gag gct 672  
 Gln Thr Ala Lys Gly Phe Lys Val Lys Leu Glu Glu His Ala Glu Ala  
 210 215 220  
 cat gtt aac cct ttg aag gtt aaa ggt ggc agc ggt ggc gac gag gtg 720  
 His Val Asn Pro Leu Lys Val Lys Gly Gly Ser Gly Gly Asp Glu Val  
 225 230 235 240  
 gac ggt acc ggt ggc agc atg gtg agt gtg att aaa cca gag atg aag 768  
 Asp Gly Thr Gly Gly Ser Met Val Ser Val Ile Lys Pro Glu Met Lys  
 245 250 255  
 atg agg tac tac atg gac ggc tcc gtc aat ggg cat gag ttc aca att 816  
 Met Arg Tyr Tyr Met Asp Gly Ser Val Asn Gly His Glu Phe Thr Ile  
 260 265 270  
 gaa ggt gaa ggc aca ggc aga cct tac gag gga cat caa gag atg aca 864  
 Glu Gly Glu Gly Thr Gly Arg Pro Tyr Glu Gly His Gln Glu Met Thr  
 275 280 285  
 cta cgc gtc aca atg gcc aag ggc ggg cca atg cct ttc gcg ttt gac 912  
 Leu Arg Val Thr Met Ala Lys Gly Gly Pro Met Pro Phe Ala Phe Asp  
 290 295 300  
 tta gtg tca cac gtg ttc tgt tac ggc cac aga cct ttt act aaa tat 960  
 Leu Val Ser His Val Phe Cys Tyr Gly His Arg Pro Phe Thr Lys Tyr  
 305 310 315 320  
 cca gaa gag ata cca gac tat ttc aaa caa gca ttt cct gaa ggc ctg 1008  
 Pro Glu Glu Ile Pro Asp Tyr Phe Lys Gln Ala Phe Pro Glu Gly Leu  
 325 330 335  
 tca tgg gaa agg tcg ttg gag ttc gaa gat ggt ggg tcc gct tca gtc 1056  
 Ser Trp Glu Arg Ser Leu Glu Phe Glu Asp Gly Gly Ser Ala Ser Val  
 340 345 350



agt gcg cat ata agc ctt aga gga aac acc ttc tac cac aaa tcc aaa 1104  
 Ser Ala His Ile Ser Leu Arg Gly Asn Thr Phe Tyr His Lys Ser Lys

355

360

365

ttt act ggg gtt aac ttt cct gcc gat ggt cct atc atg caa aac caa 1152  
 Phe Thr Gly Val Asn Phe Pro Ala Asp Gly Pro Ile Met Gln Asn Gln

370

375

380

agt gtt gat tgg gag cca tca acc gag aaa att act gcc agc gac gga 1200  
 Ser Val Asp Trp Glu Pro Ser Thr Glu Lys Ile Thr Ala Ser Asp Gly

385

390

395

400

gtt ctg aag ggt gat gtt acg atg tac cta aaa ctt gaa gga ggc ggc 1248  
 Val Leu Lys Gly Asp Val Thr Met Tyr Leu Lys Leu Glu Gly Gly Gly

405

410

415

aat cac aaa tgc caa ttc aag act act tac aag gcg gca aaa aag att 1296  
 Asn His Lys Cys Gln Phe Lys Thr Thr Tyr Lys Ala Ala Lys Lys Ile

420

425

430

ctt aaa atg cca gga agc cat tac atc agc cat cgc ctc gtc agg aaa 1344  
 Leu Lys Met Pro Gly Ser His Tyr Ile Ser His Arg Leu Val Arg Lys

435

440

445

acc gaa ggc aac att act gag ctg gta gaa gat gca gta gct cat tcc 1392  
 Thr Glu Gly Asn Ile Thr Glu Leu Val Glu Asp Ala Val Ala His Ser

450

455

460

taa

1395

<210> 37

<211> 221

<212> PRT

<213> *Montipora. sp*

<400> 37

Met	Ser	Val	Ile	Ala	Lys	Gln	Met	Thr	Tyr	Lys	Val	Tyr	Met	Ser	Gly
1				5						10				15	
Thr	Val	Asn	Gly	His	Tyr	Phe	Glu	Val	Glu	Gly	Asp	Gly	Lys	Gly	Lys
			20						25					30	
Pro	Tyr	Glu	Gly	Glu	Gln	Thr	Val	Lys	Leu	Thr	Val	Thr	Lys	Gly	Gly
			35					40						45	
Pro	Leu	Pro	Phe	Ala	Trp	Asp	Ile	Leu	Ser	Pro	Leu	Ser	Gln	Tyr	Gly
		50					55					60			
Ser	Ile	Pro	Phe	Thr	Lys	Tyr	Pro	Glu	Asp	Ile	Pro	Asp	Tyr	Val	Lys
65					70					75				80	
Gln	Ser	Phe	Pro	Glu	Gly	Tyr	Thr	Trp	Glu	Arg	Ile	Met	His	Phe	Glu
					85					90				95	
Asp	Gly	Ala	Val	Cys	Thr	Val	Ser	Asn	Asp	Ser	Ser	Ile	Gln	Gly	Asn
						100				105				110	
Cys	Phe	Ile	Tyr	Asn	Val	Lys	Ile	Ser	Gly	Val	Asn	Phe	Pro	Pro	Asn
			115						120					125	
Gly	Pro	Val	Met	Gln	Lys	Lys	Thr	Gln	Gly	Trp	Glu	Pro	Asn	Thr	Glu
		130						135						140	
Arg	Leu	Phe	Ala	Arg	Asp	Gly	Met	Leu	Ile	Gly	Asn	Asn	Phe	Met	Ala
145								150				155			160
Leu	Lys	Leu	Glu	Gly	Gly	Gly	His	Tyr	Leu	Cys	Glu	Phe	Lys	Ser	Thr
						165				170				175	
Tyr	Lys	Ala	Lys	Lys	Pro	Val	Arg	Met	Pro	Gly	Tyr	His	Tyr	Val	Asp
						180				185				190	
Arg	Lys	Leu	Asp	Val	Thr	Ser	His	Asn	Lys	Asp	Tyr	Thr	Phe	Val	Glu
						195				200				205	
Gln	Cys	Glu	Ile	Ser	Ile	Ala	Arg	His	Ser	Leu	Leu	Gly			

210	215	220
<210> 38		
<211> 666		
<212> DNA		
<213> <i>Montipora. sp</i>		
<400> 38		
atg agt gtg atc gct aaa caa atg acc tac aag gtt tat atg tca ggc 48		
Met Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly		
1	5	10
acg gtc aat gga cac tac ttt gag gtc gaa ggc gat gga aaa gga aag 96		
Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys		
20	25	30
cct tac gag ggg gag cag acg gta aag ctc act gtc acc aag ggt gga 144		
Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly		
35	40	45
cct ctg cca ttt gct tgg gat att tta tca cca ctg tct cag tac gga 192		
Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Leu Ser Gln Tyr Gly		
50	55	60
agc ata cca ttc acc aag tac cct gaa gac atc cct gat tat gta aag 240		
Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys		
65	70	75
cag tca ttc cct gag gga tat aca tgg gag agg atc atg cac ttt gaa 288		
Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met His Phe Glu		
85	90	95
gat ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac 336		
Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn		
100	105	110

tgt ttc atc tac aat gtc aaa atc tct ggt gtg aac ttt cct ccc aat 384  
 Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Val Asn Phe Pro Pro Asn

115

120

125

gga cct gtt atg cag aag aag aca cag ggc tgg gaa ccc aac act gag 432  
 Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Asn Thr Glu

130

135

140

cgt ctc ttt gca cga gat gga atg ctg ata gga aac aac ttt atg gct 480  
 Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asn Phe Met Ala

145

150

155

160

ctg aag ttg gaa gga ggt ggt cac tat ttg tgt gaa ttc aaa tct act 528  
 Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr

165

170

175

tac aag gca aag aag cct gtg agg atg cca ggg tat cac tat gtt gac 576  
 Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His Tyr Val Asp

180

185

190

cgc aaa ctg gat gta acc agt cac aac aag gat tac aca ttt gtt gag 624  
 Arg Lys Leu Asp Val Thr Ser His Asn Lys Asp Tyr Thr Phe Val Glu

195

200

205

cag tgt gaa ata tcc att gca cgc cac tct ttg ctc ggt tga 666  
 Gln Cys Glu Ile Ser Ile Ala Arg His Ser Leu Leu Gly

210

215

220

<210> 39

<211> 222

<212> PRT

<213> *Montipora. sp*

<400> 39

Met Val Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser

1	5	10	15
Gly Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly			
20	25	30	
Lys Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly			
35	40	45	
Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Leu Ser Gln Tyr			
50	55	60	
Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val			
65	70	75	80
Lys Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe			
85	90	95	
Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly			
100	105	110	
Asn Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Val Asn Phe Pro Pro			
115	120	125	
Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Ser Thr			
130	135	140	
Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp Phe Met			
145	150	155	160
Ala Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser			
165	170	175	
Thr Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His Tyr Val			
180	185	190	
Asp Arg Lys Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr Ser Val			
195	200	205	
Glu Gln Cys Glu Ile Ser Ile Ala Arg His Ser Leu Leu Gly			
210	215	220	

<210> 40

<211> 669

<212> DNA

<213> *Montipora. sp*

<400> 40

```
atg gtg agt gtg atc gct aaa caa atg acc tac aag gtt tat atg tca 48
Met Val Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser
      1              5              10              15
ggc acg gtc aat gga cac tac ttt gag gtc gaa ggc gat gga aaa gga 96
Gly Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly
              20              25              30
aag cct tac gag gga gag cag aca gta aag ctc act gtc acc aag ggt 144
Lys Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly
              35              40              45
gga cct ctg cca ttt gct tgg gat att tta tca cca ctg tct cag tac 192
Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Leu Ser Gln Tyr
              50              55              60
gga agc ata cca ttc acc aag tac cct gaa gac atc cct gat tat gta 240
Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val
              65              70              75              80
aag cag tca ttc cct gag gga tat aca tgg gag agg atc atg aac ttt 288
Lys Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ile Met Asn Phe
              85              90              95
gaa gat ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc 336
Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly
              100              105              110
aac tgt ttc atc tac aat gtc aaa atc tct ggt gtg aac ttt cct ccc 384
```

Asn Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Val Asn Phe Pro Pro  
 115 120 125  
 aat gga cct gtt atg cag aag aag aca cag ggc tgg gaa ccc agc act 432  
 Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Ser Thr  
 130 135 140  
 gag cgt ctc ttt gca cga gat gga atg ctg ata gga aac gat ttt atg 480  
 Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp Phe Met  
 145 150 155 160  
 gct ctg aag ttg gaa gga ggt ggt cac tat ttg tgt gaa ttc aaa tct 528  
 Ala Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser  
 165 170 175  
 act tac aag gca aag aag cct gtg agg atg cca ggg tat cac tat gtt 576  
 Thr Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His Tyr Val  
 180 185 190  
 gac cgc aaa ctg gat gta acc agt cac aac agg gat tac aca tct gtt 624  
 Asp Arg Lys Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr Ser Val  
 195 200 205  
 gag cag tgt gaa ata tcc att gca cgc cac tct ttg ctc ggt tga 669  
 Glu Gln Cys Glu Ile Ser Ile Ala Arg His Ser Leu Leu Gly  
 210 215 220  
 <210> 41  
 <211> 222  
 <212> PRT  
 <213> *Montipora. sp*  
 <400> 41  
 Met Val Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser  
 1 5 10 15

Gly Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly			
20	25	30	
Lys Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly			
35	40	45	
Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Leu Phe Gln Tyr			
50	55	60	
Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val			
65	70	75	80
Lys Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Thr Met Asn Phe			
85	90	95	
Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly			
100	105	110	
Asn Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Thr Asn Phe Pro Pro			
115	120	125	
Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Ser Thr			
130	135	140	
Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp Tyr Met			
145	150	155	160
Ala Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser			
165	170	175	
Thr Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His Tyr Ile			
180	185	190	
Asp Arg Lys Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr Ser Val			
195	200	205	
Glu Gln Cys Glu Ile Ala Ile Ala Arg His Ser Leu Leu Gly			
210	215	220	

<210> 42



<211> 669

<212> DNA

<213> *Montipora. sp*

<400> 42

atg gtg agt gtg atc gct aaa caa atg acc tac aag gtt tat atg tca 48

Met Val Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser

1 5 10 15

ggc acg gtc aat gga cac tac ttt gag gtc gaa ggc gat gga aaa gga 96

Gly Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly

20 25 30

aag cct tac gag gga gag cag aca gta aag ctc act gtc acc aag ggt 144

Lys Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly

35 40 45

gga cct ctg cca ttt gct tgg gat att tta tca cca ctg ttt cag tac 192

Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Leu Phe Gln Tyr

50 55 60

gga agc ata cca ttc acc aag tac cct gaa gac atc cct gat tat gta 240

Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val

65 70 75 80

aag cag tca ttc cct gag gga tat aca tgg gag agg acc atg aac ttt 288

Lys Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Thr Met Asn Phe

85 90 95

gaa gat ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc 336

Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly

100 105 110

aac tgt ttc atc tac aat gtc aaa atc tct ggt acg aac ttt cct ccc 384

Asn Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Thr Asn Phe Pro Pro

115	120	125	
aat gga cct gtt atg cag aag aag aca cag ggc tgg gaa ccc agc act 432			
Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Ser Thr			
130	135	140	
gag cgt ctc ttt gca cga gat gga atg ctg ata gga aac gat tat atg 480			
Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp Tyr Met			
145	150	155	160
gct ctg aag ttg gaa gga ggt ggt cac tat ttg tgt gaa ttt aaa tct 528			
Ala Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser			
	165	170	175
act tac aag gca aag aag cct gtg agg atg cca ggg tat cac tat att 576			
Thr Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His Tyr Ile			
180	185	190	
gac cgc aaa ctg gat gta acc agt cac aac agg gat tac aca tct gtt 624			
Asp Arg Lys Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr Ser Val			
195	200	205	
gag cag tgt gaa ata gcc att gca cgc cac tct ttg ctc ggt tga 669			
Glu Gln Cys Glu Ile Ala Ile Ala Arg His Ser Leu Leu Gly			
210	215	220	
<210> 43			
<211> 222			
<212> PRT			
<213> <i>Montipora. sp</i>			
<400> 43			
Met Val Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser			
1	5	10	15
Gly Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly			

20	25	30
Lys Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly		
35	40	45
Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Leu Met Cys Tyr		
50	55	60
Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val		
65	70	75
Lys Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Thr Met Asn Phe		
85	90	95
Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly		
100	105	110
Asn Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Thr Asn Phe Pro Pro		
115	120	125
Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Ser Thr		
130	135	140
Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp Tyr Met		
145	150	155
Ala Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser		
165	170	175
Thr Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His Tyr Ile		
180	185	190
Asp Arg Lys Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr Ser Val		
195	200	205
Glu Gln Cys Glu Ile Ala Ile Ala Arg His Ser Leu Leu Gly		
210	215	220

<210> 44

<211> 669

<212> DNA

<213> *Montipora. sp*

<400> 44

```
atg gtg agt gtg atc gct aaa caa atg acc tac aag gtt tat atg tca 48
Met Val Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser
      1              5              10              15
ggc acg gtc aat gga cac tac ttt gag gtc gaa ggc gat gga aaa gga 96
Gly Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly
              20              25              30
aag cct tac gag gga gag cag aca gta aag ctc act gtc acc aag ggt 144
Lys Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly
              35              40              45
gga cct ctg cca ttt gct tgg gat att tta tca cca ctg atg tgt tac 192
Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Leu Met Cys Tyr
              50              55              60
gga agc ata cca ttc acc aag tac cct gaa gac atc cct gat tat gta 240
Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val
              65              70              75              80
aag cag tca ttc cct gag gga tat aca tgg gag agg acc atg aac ttt 288
Lys Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Thr Met Asn Phe
              85              90              95
gaa gat ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc 336
Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly
              100              105              110
aac tgt ttc atc tac aat gtc aaa atc tct ggt acg aac ttt cct ccc 384
Asn Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Thr Asn Phe Pro Pro
              115              120              125
```

aat gga cct gtt atg cag aag aag aca cag ggc tgg gaa ccc agc act 432  
 Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Ser Thr

130

135

140

gag cgt ctc ttt gca cga gat gga atg ctg ata gga aac gat tat atg 480  
 Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp Tyr Met

145

150

155

160

gct ctg aag ttg gaa gga ggt ggt cac tat ttg tgt gaa ttt aaa tct 528  
 Ala Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser

165

170

175

act tac aag gca aag aag cct gtg agg atg cca ggg tat cac tat att 576  
 Thr Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His Tyr Ile

180

185

190

gac cgc aaa ctg gat gta acc agt cac aac agg gat tac aca tct gtt 624  
 Asp Arg Lys Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr Ser Val

195

200

205

gag cag tgt gaa ata gcc att gca cgc cac tct ttg ctc ggt tga 669  
 Glu Gln Cys Glu Ile Ala Ile Ala Arg His Ser Leu Leu Gly

210

215

220

<210> 45

<211> 255

<212> PRT

<213> *Montipora. sp*

<400> 45

Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr

1

5

10

15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp

20

25

30

Pro Met Val Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met			
35	40	45	
Ser Gly Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys			
50	55	60	
Gly Lys Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys			
65	70	75	80
Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe Gln			
85	90	95	
Tyr Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr			
100	105	110	
Phe Lys Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ser Met Asn			
115	120	125	
Phe Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln			
130	135	140	
Gly Asn Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Glu Asn Phe Pro			
145	150	155	160
Pro Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Ser			
165	170	175	
Thr Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp Tyr			
180	185	190	
Met Ala Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys			
195	200	205	
Ser Thr Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Arg His Glu			
210	215	220	
Ile Asp Arg Lys Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr Ser			
225	230	235	240
Val Glu Gln Cys Glu Ile Ala Ile Ala Arg His Ser Leu Leu Gly			



ttc aag cag tca ttc cct gag gga tat aca tgg gag agg agc atg aac 384  
 Phe Lys Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ser Met Asn  
           115                          120                          125  
 ttt gaa gat ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa 432  
 Phe Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln  
           130                          135                          140  
 ggc aac tgt ttc atc tac aat gtc aaa atc tct ggt gag aac ttt cct 480  
 Gly Asn Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Glu Asn Phe Pro  
 145                          150                          155                          160  
 ccc aat gga cct gtt atg cag aag aag aca cag ggc tgg gaa ccc agc 528  
 Pro Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Ser  
                           165                          170                          175  
 act gag cgt ctc ttt gca cga gat gga atg ctg ata gga aac gat tat 576  
 Thr Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp Tyr  
                           180                          185                          190  
 atg gct ctg aag ttg gaa gga ggt ggt cac tat ttg tgt gaa ttt aaa 624  
 Met Ala Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys  
           195                          200                          205  
 tct act tac aag gca aag aag cct gtg agg atg cca ggg cgc cac gag 672  
 Ser Thr Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Arg His Glu  
           210                          215                          220  
 att gac cgc aaa ctg gat gta acc agt cac aac agg gat tac aca tct 720  
 Ile Asp Arg Lys Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr Ser  
 225                          230                          235                          240  
 gtt gag cag tgt gaa ata gcc att gca cgc cac tct ttg ctc ggt 765  
 Val Glu Gln Cys Glu Ile Ala Ile Ala Arg His Ser Leu Leu Gly  
                           245                          250                          255



<210> 47

<211> 255

<212> PRT

<213> *Montipora. sp*

<400> 47

Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr  
1 5 10 15  
Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp  
20 25 30  
Pro Met Val Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met  
35 40 45  
Ser Gly Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys  
50 55 60  
Gly Lys Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys  
65 70 75 80  
Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Leu Gln  
85 90 95  
Tyr Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr  
100 105 110  
Phe Lys Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ser Met Asn  
115 120 125  
Phe Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln  
130 135 140  
Gly Asn Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Glu Asn Phe Pro  
145 150 155 160  
Pro Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Ser  
165 170 175

Thr	Glu	Arg	Leu	Phe	Ala	Arg	Asp	Gly	Met	Leu	Ile	Gly	Asn	Asp	Tyr
			180					185					190		
Met	Ala	Leu	Lys	Leu	Glu	Gly	Gly	Gly	His	Tyr	Leu	Cys	Glu	Phe	Lys
		195					200					205			
Ser	Thr	Tyr	Lys	Ala	Lys	Lys	Pro	Val	Arg	Met	Pro	Gly	Arg	His	Glu
	210					215					220				
Ile	Asp	Arg	Lys	Leu	Asp	Val	Thr	Ser	His	Asn	Arg	Asp	Tyr	Thr	Ser
225				230					235					240	
Val	Glu	Gln	Cys	Glu	Ile	Ala	Ile	Ala	Arg	His	Ser	Leu	Leu	Gly	
			245					250					255		

<210> 48

<211> 765

<212> DNA

<213> *Montipora. sp*

<400> 48

atg cgg ggt tct cat cat cat cat cat cat ggt atg gct agc atg act 48															
Met	Arg	Gly	Ser	His	His	His	His	His	His	Gly	Met	Ala	Ser	Met	Thr
1				5						10				15	
ggt gga cag caa atg ggt cgg gat ctg tac gac gat gac gat aag gat 96															
Gly	Gly	Gln	Gln	Met	Gly	Arg	Asp	Leu	Tyr	Asp	Asp	Asp	Asp	Lys	Asp
			20					25					30		
ccc atg gtg agt gtg atc gct aaa caa atg acc tac aag gtt tat atg 144															
Pro	Met	Val	Ser	Val	Ile	Ala	Lys	Gln	Met	Thr	Tyr	Lys	Val	Tyr	Met
		35					40					45			
tca ggc acg gtc aat gga cac tac ttt gag gtc gaa ggc gat gga aaa 192															
Ser	Gly	Thr	Val	Asn	Gly	His	Tyr	Phe	Glu	Val	Glu	Gly	Asp	Gly	Lys
		50				55						60			

gga aag cct tac gag gga gag cag aca gta aag ctc act gtc acc aag 240  
 Gly Lys Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys  
 65 70 75 80  
 ggt gga cct ctg cca ttt gct tgg gat att tta tca cca cag ctt cag 288  
 Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Leu Gln  
 85 90 95  
 tac gga agc ata cca ttc acc aag tac cct gaa gac atc cct gat tat 336  
 Tyr Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr  
 100 105 110  
 ttc aag cag tca ttc cct gag gga tat aca tgg gag agg agc atg aac 384  
 Phe Lys Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Ser Met Asn  
 115 120 125  
 ttt gaa gat ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa 432  
 Phe Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln  
 130 135 140  
 ggc aac tgt ttc atc tac aat gtc aaa atc tct ggt gag aac ttt cct 480  
 Gly Asn Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Glu Asn Phe Pro  
 145 150 155 160  
 ccc aat gga cct gtt atg cag aag aag aca cag ggc tgg gaa ccc agc 528  
 Pro Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Ser  
 165 170 175  
 act gag cgt ctc ttt gca cga gat gga atg ctg ata gga aac gat tat 576  
 Thr Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp Tyr  
 180 185 190  
 atg gct ctg aag ttg gaa gga ggt ggt cac tat ttg tgt gaa ttt aaa 624  
 Met Ala Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys  
 195 200 205

tct act tac aag gca aag aag cct gtg agg atg cca ggg cgc cac gag 672

Ser Thr Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Arg His Glu

210

215

220

att gac cgc aaa ctg gat gta acc agt cac aac agg gat tac aca tct 720

Ile Asp Arg Lys Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr Ser

225

230

235

240

gtt gag cag tgt gaa ata gcc att gca cgc cac tct ttg ctc ggt 765

Val Glu Gln Cys Glu Ile Ala Ile Ala Arg His Ser Leu Leu Gly

245

250

255

<210> 49

<211> 747

<212> PRT

<213> *Montipora. sp*

<400> 49

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu

1

5

10

15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly

20

25

30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile

35

40

45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr

50

55

60

Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys

65

70

75

80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu

85

90

95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu

100	105	110
Val Lys Phe Glu Gly Asp Thr Leu	Val Asn Arg Ile Glu Leu Lys Gly	
115	120	125
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr		
130	135	140
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn		
145	150	155
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser		
165	170	175
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly		
180	185	190
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu		
195	200	205
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe		
210	215	220
Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser		
225	230	235
Gly Leu Arg Ser Arg Ala Gln Ala Ser Asn Ser Ala Val Asp Gly Thr		
245	250	255
Ala Gly Pro Leu Tyr Asp Glu Val Asp Lys Asp Pro Met Ala Ser Ser		
260	265	270
Glu Asp Val Ile Lys Glu Phe Met Arg Phe Lys Val Arg Met Glu Gly		
275	280	285
Ser Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu Gly Glu Gly Arg		
290	295	300
Pro Tyr Glu Gly Thr Gln Thr Ala Lys Leu Lys Val Thr Lys Gly Gly		
305	310	315
		320

Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe Gln Tyr Gly  
                             325                            330                            335  
 Ser Lys Ala Tyr Val Lys His Pro Ala Asp Ile Pro Asp Tyr Leu Lys  
                             340                            345                            350  
 Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val Met Asn Phe Glu  
                             355                            360                            365  
 Asp Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser Leu Gln Asp Gly  
                             370                            375                            380  
 Glu Phe Ile Tyr Lys Val Lys Leu Arg Gly Thr Asn Phe Pro Ser Asp  
 385                            390                            395                            400  
 Gly Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu Ala Ser Thr Glu  
                             405                            410                            415  
 Arg Met Tyr Pro Glu Asp Gly Ala Leu Lys Gly Glu Ile Lys Met Arg  
                             420                            425                            430  
 Leu Lys Leu Lys Asp Gly Gly His Tyr Asp Ala Glu Val Lys Thr Thr  
                             435                            440                            445  
 Tyr Met Ala Lys Lys Pro Val Gln Leu Pro Gly Ala Tyr Lys Thr Asp  
                             450                            455                            460  
 Ile Lys Leu Asp Ile Thr Ser His Asn Glu Asp Tyr Thr Ile Val Glu  
 465                            470                            475                            480  
 Gln Tyr Glu Arg Ala Glu Gly Arg His Ser Thr Gly Ala Ser Gly Leu  
                             485                            490                            495  
 Arg Ser Arg Ala Gln Ala Ser Asn Ser Ala Val Asp Gly Thr Ala Gly  
                             500                            505                            510  
 Pro Leu Tyr Asp Glu Val Gly Lys Asp Pro Met Ala Ser Ser Glu Asp  
                             515                            520                            525  
 Val Ile Lys Glu Phe Met Arg Phe Lys Val Arg Met Glu Gly Ser Val

530	535	540	
Asn Gly His Glu Phe Glu Ile Glu Gly Glu Gly Glu Gly Arg Pro Tyr			
545	550	555	560
Glu Gly Thr Gln Thr Ala Lys Leu Lys Val Thr Lys Gly Gly Pro Leu			
	565	570	575
Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe Gln Tyr Gly Ser Lys			
	580	585	590
Ala Tyr Val Lys His Pro Ala Asp Ile Pro Asp Tyr Leu Lys Leu Ser			
	595	600	605
Phe Pro Glu Gly Phe Lys Trp Glu Arg Val Met Asn Phe Glu Asp Gly			
	610	615	620
Gly Val Val Thr Val Thr Gln Asp Ser Ser Leu Gln Asp Gly Glu Phe			
625	630	635	640
Ile Tyr Lys Val Lys Leu Arg Gly Thr Asn Phe Pro Ser Asp Gly Pro			
	645	650	655
Val Met Gln Lys Lys Thr Met Gly Trp Glu Ala Ser Thr Glu Arg Met			
	660	665	670
Tyr Pro Glu Asp Gly Ala Leu Lys Gly Glu Ile Lys Met Arg Leu Lys			
	675	680	685
Leu Lys Asp Gly Gly His Tyr Asp Ala Glu Val Lys Thr Thr Tyr Met			
	690	695	700
Ala Lys Lys Pro Val Gln Leu Pro Gly Ala Tyr Lys Thr Asp Ile Lys			
705	710	715	720
Leu Asp Ile Thr Ser His Asn Glu Asp Tyr Thr Ile Val Glu Gln Tyr			
	725	730	735
Glu Arg Ala Glu Gly Arg His Ser Thr Gly Ala			
	740	745	

<210> 50

<211> 2241

<212> DNA

<213> *Montipora. sp*

<400> 50

```
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
      1              5              10              15
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
              20              25              30
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
              35              40              45
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
              50              55              60
ctg acc tac ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg aag 240
Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
              65              70              75              80
cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
              85              90              95
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
              100             105             110
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
```



Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly  
115 120 125  
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432  
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr  
130 135 140  
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac 480  
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn  
145 150 155 160  
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc 528  
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser  
165 170 175  
gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc 576  
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly  
180 185 190  
ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc ctg 624  
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu  
195 200 205  
agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc 672  
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe  
210 215 220  
gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag tcc 720  
Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser  
225 230 235 240  
gga ctc aga tct cga gct caa gct tcg aat tct gca gtc gac ggt acc 768  
Gly Leu Arg Ser Arg Ala Gln Ala Ser Asn Ser Ala Val Asp Gly Thr  
245 250 255  
gcg ggc ccg ctg tac gac gaa gtc gat aag gat ccg atg gcc tcc tcc 816

Ala Gly Pro Leu Tyr Asp Glu Val Asp Lys Asp Pro Met Ala Ser Ser  
                   260                                  265                                  270  
 gag gac gtc atc aag gag ttc atg cgc ttc aag gtg cgc atg gag ggc 864  
 Glu Asp Val Ile Lys Glu Phe Met Arg Phe Lys Val Arg Met Glu Gly  
                   275                                  280                                  285  
 tcc gtg aac ggc cac gag ttc gag atc gag ggc gag ggc gag ggc cgc 912  
 Ser Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu Gly Glu Gly Arg  
                   290                                  295                                  300  
 ccc tac gag ggc acc cag acc gcc aag ctg aag gtg acc aag ggc ggc 960  
 Pro Tyr Glu Gly Thr Gln Thr Ala Lys Leu Lys Val Thr Lys Gly Gly  
 305                                  310                                  315                                  320  
 ccc ctg ccc ttc gcc tgg gac atc ctg tcc cct cag ttc cag tac ggc 1008  
 Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe Gln Tyr Gly  
                                   325                                  330                                  335  
 tcc aag gcc tac gtg aag cac ccc gcc gac atc ccc gac tac ttg aag 1056  
 Ser Lys Ala Tyr Val Lys His Pro Ala Asp Ile Pro Asp Tyr Leu Lys  
                   340                                  345                                  350  
 ctg tcc ttc ccc gag ggc ttc aag tgg gag cgc gtg atg aac ttc gag 1104  
 Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val Met Asn Phe Glu  
                   355                                  360                                  365  
 gac ggc ggc gtg gtg acc gtg acc cag gac tcc tcc ctg cag gac ggc 1152  
 Asp Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser Leu Gln Asp Gly  
                   370                                  375                                  380  
 gag ttc atc tac aag gtg aag ctg cgc ggc acc aac ttc ccc tcc gac 1200  
 Glu Phe Ile Tyr Lys Val Lys Leu Arg Gly Thr Asn Phe Pro Ser Asp  
 385                                  390                                  395                                  400  
 ggc ccc gta atg cag aag aag acc atg ggc tgg gag gcc tcc acc gag 1248

Gly Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu Ala Ser Thr Glu  
 405 410 415  
 cgg atg tac ccc gag gac ggc gcc ctg aag ggc gag atc aag atg agg 1296  
 Arg Met Tyr Pro Glu Asp Gly Ala Leu Lys Gly Glu Ile Lys Met Arg  
 420 425 430  
 ctg aag ctg aag gac ggc ggc cac tac gac gcc gag gtc aag acc acc 1344  
 Leu Lys Leu Lys Asp Gly Gly His Tyr Asp Ala Glu Val Lys Thr Thr  
 435 440 445  
 tac atg gcc aag aag ccc gtg cag ctg ccc ggc gcc tac aag acc gac 1392  
 Tyr Met Ala Lys Lys Pro Val Gln Leu Pro Gly Ala Tyr Lys Thr Asp  
 450 455 460  
 atc aag ctg gac atc acc tcc cac aac gag gac tac acc atc gtg gaa 1440  
 Ile Lys Leu Asp Ile Thr Ser His Asn Glu Asp Tyr Thr Ile Val Glu  
 465 470 475 480  
 cag tac gag cgc gcc gag ggc cgc cac tcc acc ggc gcc tcc gga ctc 1488  
 Gln Tyr Glu Arg Ala Glu Gly Arg His Ser Thr Gly Ala Ser Gly Leu  
 485 490 495  
 aga tct cga gct caa gct tcg aat tct gca gtc gac ggt acc gcg ggc 1536  
 Arg Ser Arg Ala Gln Ala Ser Asn Ser Ala Val Asp Gly Thr Ala Gly  
 500 505 510  
 ccg ctg tac gac gaa gtc ggt aag gat ccg atg gcc tcc tcc gag gac 1584  
 Pro Leu Tyr Asp Glu Val Gly Lys Asp Pro Met Ala Ser Ser Glu Asp  
 515 520 525  
 gtc atc aag gag ttc atg cgc ttc aag gtg cgc atg gag ggc tcc gtg 1632  
 Val Ile Lys Glu Phe Met Arg Phe Lys Val Arg Met Glu Gly Ser Val  
 530 535 540  
 aac ggc cac gag ttc gag atc gag ggc gag ggc gag ggc cgc ccc tac 1680

Asn Gly His Glu Phe Glu Ile Glu Gly Glu Gly Glu Gly Arg Pro Tyr  
 545                      550                      555                      560  
 gag ggc acc cag acc gcc aag ctg aag gtg acc aag ggc ggc ccc ctg 1728  
 Glu Gly Thr Gln Thr Ala Lys Leu Lys Val Thr Lys Gly Gly Pro Leu  
                          565                      570                      575  
 ccc ttc gcc tgg gac atc ctg tcc cct cag ttc cag tac ggc tcc aag 1776  
 Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe Gln Tyr Gly Ser Lys  
                          580                      585                      590  
 gcc tac gtg aag cac ccc gcc gac atc ccc gac tac ttg aag ctg tcc 1824  
 Ala Tyr Val Lys His Pro Ala Asp Ile Pro Asp Tyr Leu Lys Leu Ser  
                          595                      600                      605  
 ttc ccc gag ggc ttc aag tgg gag cgc gtg atg aac ttc gag gac ggc 1872  
 Phe Pro Glu Gly Phe Lys Trp Glu Arg Val Met Asn Phe Glu Asp Gly  
                          610                      615                      620  
 ggc gtg gtg acc gtg acc cag gac tcc tcc ctg cag gac ggc gag ttc 1920  
 Gly Val Val Thr Val Thr Gln Asp Ser Ser Leu Gln Asp Gly Glu Phe  
 625                      630                      635                      640  
 atc tac aag gtg aag ctg cgc ggc acc aac ttc ccc tcc gac ggc ccc 1968  
 Ile Tyr Lys Val Lys Leu Arg Gly Thr Asn Phe Pro Ser Asp Gly Pro  
                          645                      650                      655  
 gta atg cag aag aag acc atg ggc tgg gag gcc tcc acc gag cgg atg 2016  
 Val Met Gln Lys Lys Thr Met Gly Trp Glu Ala Ser Thr Glu Arg Met  
                          660                      665                      670  
 tac ccc gag gac ggc gcc ctg aag ggc gag atc aag atg agg ctg aag 2064  
 Tyr Pro Glu Asp Gly Ala Leu Lys Gly Glu Ile Lys Met Arg Leu Lys  
                          675                      680                      685  
 ctg aag gac ggc ggc cac tac gac gcc gag gtc aag acc acc tac atg 2112

Leu Lys Asp Gly Gly His Tyr Asp Ala Glu Val Lys Thr Thr Tyr Met  
 690 695 700  
 gcc aag aag ccc gtg cag ctg ccc ggc gcc tac aag acc gac atc aag 2160  
 Ala Lys Lys Pro Val Gln Leu Pro Gly Ala Tyr Lys Thr Asp Ile Lys  
 705 710 715 720  
 ctg gac atc acc tcc cac aac gag gac tac acc atc gtg gaa cag tac 2208  
 Leu Asp Ile Thr Ser His Asn Glu Asp Tyr Thr Ile Val Glu Gln Tyr  
 725 730 735  
 gag cgc gcc gag ggc cgc cac tcc acc ggc gcc 2241  
 Glu Arg Ala Glu Gly Arg His Ser Thr Gly Ala  
 740 745  
 <210> 51  
 <211> 507  
 <212> PRT  
 <213> *Montipora. sp*  
 <400> 51  
 Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr  
 1 5 10 15  
 Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp  
 20 25 30  
 Pro Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile  
 35 40 45  
 Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser  
 50 55 60  
 Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe  
 65 70 75 80  
 Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr

	85	90	95
Thr Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met			
	100	105	110
Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln			
	115	120	125
Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala			
	130	135	140
Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys			
	145	150	155
Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu			
	165	170	175
Tyr Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys			
	180	185	190
Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly			
	195	200	205
Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp			
	210	215	220
Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala			
	225	230	235
Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu			
	245	250	255
Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys			
	260	265	270
Ser Ser Ser Glu Leu Ser Gly Asp Glu Val Asp Gly Thr Met Val Ser			
	275	280	285
Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr Val			
	290	295	300

Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro Tyr			
305	310	315	320
Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro Leu			
	325	330	335
Pro Phe Ala Trp Asp Ile Leu Ser Pro Leu Phe Gln Tyr Gly Ser Ile			
	340	345	350
Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln Ser			
	355	360	365
Phe Pro Glu Gly Tyr Thr Trp Glu Arg Thr Met Asn Phe Glu Asp Gly			
	370	375	380
Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys Phe			
385	390	395	400
Ile Tyr Asn Val Lys Ile Ser Gly Thr Asn Phe Pro Pro Asn Gly Pro			
	405	410	415
Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Ser Thr Glu Arg Leu			
	420	425	430
Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp Tyr Met Ala Leu Lys			
	435	440	445
Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr Lys			
	450	455	460
Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His Tyr Ile Asp Arg Lys			
465	470	475	480
Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr Ser Val Glu Gln Cys			
	485	490	495
Glu Ile Ala Ile Ala Arg His Ser Leu Leu Gly			
	500	505	

<210> 52

<211> 1521

<212> DNA

<213> *Montipora. sp*

<400> 52

```
atg cgg ggt tct cat cat cat cat cat cat ggt atg gct agc atg act 48
Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
      1              5              10              15
ggt gga cag caa atg ggt cgg gat ctg tac gac gat gac gat aag gat 96
Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
              20              25              30
ccc atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc 144
Pro Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile
              35              40              45
ctg gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc 192
Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser
              50              55              60
ggc gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc 240
Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe
              65              70              75              80
atc tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc 288
Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr
              85              90              95
acc ctg acc tgg ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg 336
Thr Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met
              100              105              110
aag cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag 384
Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln
```



115	120	125	
gag cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc 432			
Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala			
130	135	140	
gag gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag 480			
Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys			
145	150	155	160
ggc atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag 528			
Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu			
	165	170	175
tac aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag 576			
Tyr Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys			
	180	185	190
aac ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc 624			
Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly			
195	200	205	
agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac 672			
Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp			
210	215	220	
ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc 720			
Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala			
225	230	235	240
ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag 768			
Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu			
	245	250	255
ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag 816			
Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys			

260	265	270	
tcc tcg tcc gag ctc agc gga gat gag gtc gat ggt acc atg gtg agt	864		
Ser Ser Ser Glu Leu Ser Gly Asp Glu Val Asp Gly Thr Met Val Ser			
275	280	285	
gtg atc gct aaa caa atg acc tac aag gtt tat atg tca ggc acg gtc	912		
Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met Ser Gly Thr Val			
290	295	300	
aat gga cac tac ttt gag gtc gaa ggc gat gga aaa gga aag cct tac	960		
Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys Gly Lys Pro Tyr			
305	310	315	320
gag gga gag cag aca gta aag ctc act gtc acc aag ggt gga cct ctg	1008		
Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys Gly Gly Pro Leu			
325	330	335	
cca ttt gct tgg gat att tta tca cca ctg ttt cag tac gga agc ata	1056		
Pro Phe Ala Trp Asp Ile Leu Ser Pro Leu Phe Gln Tyr Gly Ser Ile			
340	345	350	
cca ttc acc aag tac cct gaa gac atc cct gat tat gta aag cag tca	1104		
Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr Val Lys Gln Ser			
355	360	365	
ttc cct gag gga tat aca tgg gag agg acc atg aac ttt gaa gat ggt	1152		
Phe Pro Glu Gly Tyr Thr Trp Glu Arg Thr Met Asn Phe Glu Asp Gly			
370	375	380	
gca gtg tgt act gtc agc aat gat tcc agc atc caa ggc aac tgt ttc	1200		
Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln Gly Asn Cys Phe			
385	390	395	400
atc tac aat gtc aaa atc tct ggt acg aac ttt cct ccc aat gga cct	1248		
Ile Tyr Asn Val Lys Ile Ser Gly Thr Asn Phe Pro Pro Asn Gly Pro			

405	410	415	
gtt atg cag aag aag aca cag ggc tgg gaa ccc agc act gag cgt ctc 1296			
Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Ser Thr Glu Arg Leu			
420	425	430	
ttt gca cga gat gga atg ctg ata gga aac gat tat atg gct ctg aag 1344			
Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp Tyr Met Ala Leu Lys			
435	440	445	
ttg gaa gga ggt ggt cac tat ttg tgt gaa ttt aaa tct act tac aag 1392			
Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys Ser Thr Tyr Lys			
450	455	460	
gca aag aag cct gtg agg atg cca ggg tat cac tat att gac cgc aaa 1440			
Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His Tyr Ile Asp Arg Lys			
465	470	475	480
ctg gat gta acc agt cac aac agg gat tac aca tct gtt gag cag tgt 1488			
Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr Ser Val Glu Gln Cys			
485	490	495	
gaa ata gcc att gca cgc cac tct ttg ctc ggt			1521
Glu Ile Ala Ile Ala Arg His Ser Leu Leu Gly			

500	505	
<210> 53		
<211> 507		
<212> PRT		
<213> <i>Montipora. sp</i>		
<400> 53		
Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr		
1	5	10
15		
Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp		

	20	25	30
Pro Met Val Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met			
35	40	45	
Ser Gly Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys			
50	55	60	
Gly Lys Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys			
65	70	75	80
Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Leu Phe Gln			
85	90	95	
Tyr Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr			
100	105	110	
Val Lys Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Thr Met Asn			
115	120	125	
Phe Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln			
130	135	140	
Gly Asn Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Thr Asn Phe Pro			
145	150	155	160
Pro Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Ser			
165	170	175	
Thr Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp Tyr			
180	185	190	
Met Ala Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys			
195	200	205	
Ser Thr Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His Tyr			
210	215	220	
Ile Asp Arg Lys Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr Ser			
225	230	235	240

Val Glu Gln Cys Glu Ile Ala Ile Ala Arg His Ser Leu Leu Gly Ser			
245	250	255	
Ser Ser Glu Leu Ser Gly Asp Glu Val Asp Gly Thr Met Val Ser Lys			
260	265	270	
Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp			
275	280	285	
Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly			
290	295	300	
Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly			
305	310	315	320
Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly			
325	330	335	
Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe			
340	345	350	
Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe			
355	360	365	
Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu			
370	375	380	
Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys			
385	390	395	400
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser			
405	410	415	
His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala			
420	425	430	
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala			
435	440	445	
Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu			

450                      455                      460  
 Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro  
 465                      470                      475                      480  
 Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala  
                          485                      490                      495  
 Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
                          500                      505

<210> 54

<211> 1521

<212> DNA

<213> *Montipora. sp*

<400> 54

atg cgg ggt tct cat cat cat cat cat cat ggt atg gct agc atg act 48  
 Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr  
   1                      5                      10                      15  
 ggt gga cag caa atg ggt cgg gat ctg tac gac gat gac gat aag gat 96  
 Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp  
                          20                      25                      30  
 ccc atg gtg agt gtg atc gct aaa caa atg acc tac aag gtt tat atg 144  
 Pro Met Val Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr Met  
                          35                      40                      45  
 tca ggc acg gtc aat gga cac tac ttt gag gtc gaa ggc gat gga aaa 192  
 Ser Gly Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly Lys  
                          50                      55                      60  
 gga aag cct tac gag gga gag cag aca gta aag ctc act gtc acc aag 240  
 Gly Lys Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr Lys  
   65                      70                      75                      80

ggt gga cct ctg cca ttt gct tgg gat att tta tca cca ctg ttt cag 288  
 Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Leu Phe Gln  
                     85                    90                    95  
 tac gga agc ata cca ttc acc aag tac cct gaa gac atc cct gat tat 336  
 Tyr Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp Tyr  
                     100                    105                    110  
 gta aag cag tca ttc cct gag gga tat aca tgg gag agg acc atg aac 384  
 Val Lys Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Thr Met Asn  
                     115                    120                    125  
 ttt gaa gat ggt gca gtg tgt act gtc agc aat gat tcc agc atc caa 432  
 Phe Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile Gln  
                     130                    135                    140  
 ggc aac tgt ttc atc tac aat gtc aaa atc tct ggt acg aac ttt cct 480  
 Gly Asn Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Thr Asn Phe Pro  
                     145                    150                    155                    160  
 ccc aat gga cct gtt atg cag aag aag aca cag ggc tgg gaa ccc agc 528  
 Pro Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro Ser  
                     165                    170                    175  
 act gag cgt ctc ttt gca cga gat gga atg ctg ata gga aac gat tat 576  
 Thr Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp Tyr  
                     180                    185                    190  
 atg gct ctg aag ttg gaa gga ggt ggt cac tat ttg tgt gaa ttt aaa 624  
 Met Ala Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe Lys  
                     195                    200                    205  
 tct act tac aag gca aag aag cct gtg agg atg cca ggg tat cac tat 672  
 Ser Thr Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His Tyr  
                     210                    215                    220

att gac cgc aaa ctg gat gta acc agt cac aac agg gat tac aca tct 720  
 Ile Asp Arg Lys Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr Ser  
 225                      230                      235                      240  
 gtt gag cag tgt gaa ata gcc att gca cgc cac tct ttg ctc ggt tcc 768  
 Val Glu Gln Cys Glu Ile Ala Ile Ala Arg His Ser Leu Leu Gly Ser  
                          245                      250                      255  
 tcg tcc gag ctc agc gga gat gag gtc gat ggt acc atg gtg agc aag 816  
 Ser Ser Glu Leu Ser Gly Asp Glu Val Asp Gly Thr Met Val Ser Lys  
                          260                      265                      270  
 ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc gag ctg gac 864  
 Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp  
                          275                      280                      285  
 ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag ggc gag ggc 912  
 Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly  
                          290                      295                      300  
 gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc 960  
 Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly  
 305                      310                      315                      320  
 aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg acc tgg ggc 1008  
 Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly  
                          325                      330                      335  
 gtg cag tgc ttc agc cgc tac ccc gac cac atg aag cag cac gac ttc 1056  
 Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe  
                          340                      345                      350  
 ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc 1104  
 Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe  
                          355                      360                      365



ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag 1152  
 Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu  
 370 375 380  
 ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag 1200  
 Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys  
 385 390 395 400  
 gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac tac atc agc 1248  
 Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser  
 405 410 415  
 cac aac gtc tat atc acc gcc gac aag cag aag aac ggc atc aag gcc 1296  
 His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala  
 420 425 430  
 aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc 1344  
 Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala  
 435 440 445  
 gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg 1392  
 Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu  
 450 455 460  
 ccc gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc 1440  
 Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro  
 465 470 475 480  
 aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc 1488  
 Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala  
 485 490 495  
 ggg atc act ctc ggc atg gac gag ctg tac aag 1521  
 Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys  
 500 505

<210> 55

<211> 411

<212> PRT

<213> *Montipora. sp*

<400> 55

Met	Arg	Gly	Ser	His	His	His	His	His	His	Gly	Met	Ala	Ser	Met	Thr
1				5						10				15	
Gly	Gly	Gln	Gln	Met	Gly	Arg	Asp	Leu	Tyr	Asp	Asp	Asp	Asp	Lys	Asp
				20				25						30	
Pro	Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile
				35				40						45	
Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Arg	Phe	Ser	Val	Ser
				50				55						60	
Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe
				65				70						75	
Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr
				85						90				95	
Thr	Leu	Thr	Trp	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met
				100						105				110	
Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln
				115						120				125	
Glu	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala
				130						135				140	
Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys
				145						150				155	
Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu
				165						170				175	

Tyr Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys			
180	185	190	
Asn Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu Asp Gly			
195	200	205	
Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp			
210	215	220	
Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala			
225	230	235	240
Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu			
245	250	255	
Phe Val Thr Ala Ala Arg Met His Asp Gln Leu Thr Glu Glu Gln Ile			
260	265	270	
Ala Glu Phe Lys Glu Ala Phe Ser Leu Phe Asp Lys Asp Gly Asp Gly			
275	280	285	
Thr Ile Thr Thr Lys Glu Leu Gly Thr Val Met Arg Ser Leu Gly Gln			
290	295	300	
Asn Pro Thr Glu Ala Glu Leu Gln Asp Met Ile Asn Glu Val Asp Ala			
305	310	315	320
Asp Gly Asn Gly Thr Ile Tyr Phe Pro Glu Phe Leu Thr Met Met Ala			
325	330	335	
Arg Lys Met Lys Asp Thr Asp Ser Glu Glu Glu Ile Arg Glu Ala Phe			
340	345	350	
Arg Val Phe Asp Lys Asp Gly Asn Gly Tyr Ile Ser Ala Ala Glu Leu			
355	360	365	
Arg His Val Met Thr Asn Leu Gly Glu Lys Leu Thr Asp Glu Glu Val			
370	375	380	
Asp Glu Met Ile Arg Glu Ala Asp Ile Asp Gly Asp Gly Gln Val Asn			

385 390 395 400

Tyr Glu Glu Phe Val Gln Met Met Thr Ala Lys

405 410

<210> 56

<211> 1233

<212> DNA

<213> *Montipora. sp*

<400> 56

atg cgg ggt tct cat cat cat cat cat cat ggt atg gct agc atg act 48

Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr

1 5 10 15

ggt gga cag caa atg ggt cgg gat ctg tac gac gat gac gat aag gat 96

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp

20 25 30

ccc atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc 144

Pro Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile

35 40 45

ctg gtc gag ctg gac ggc gac gta aac ggc cac agg ttc agc gtg tcc 192

Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Arg Phe Ser Val Ser

50 55 60

ggc gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc 240

Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe

65 70 75 80

atc tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc 288

Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr

85 90 95

acc ctg acc tgg ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg 336

Thr Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met  
 100 105 110  
 aag cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag 384  
 Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln  
 115 120 125  
 gag cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc 432  
 Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala  
 130 135 140  
 gag gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag 480  
 Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys  
 145 150 155 160  
 ggc atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag 528  
 Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu  
 165 170 175  
 tac aac tat atc agc cac aac gtc tat atc acc gcc gac aag cag aag 576  
 Tyr Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys  
 180 185 190  
 aac ggc atc aag gcc cac ttc aag atc cgc cac aac atc gag gac ggc 624  
 Asn Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu Asp Gly  
 195 200 205  
 agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac 672  
 Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp  
 210 215 220  
 ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc 720  
 Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala  
 225 230 235 240  
 ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag 768

Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu  
                             245                            250                            255  
 ttc gtg acc gcc gcc cgc atg cat gac caa ctg aca gaa gag cag att 816  
 Phe Val Thr Ala Ala Arg Met His Asp Gln Leu Thr Glu Glu Gln Ile  
                             260                            265                            270  
 gca gag ttc aaa gaa gcc ttc tca tta ttc gac aag gat ggg gac ggc 864  
 Ala Glu Phe Lys Glu Ala Phe Ser Leu Phe Asp Lys Asp Gly Asp Gly  
                             275                            280                            285  
 acc atc acc aca aag gaa ctt ggc acc gtt atg agg tcg ctt gga caa 912  
 Thr Ile Thr Thr Lys Glu Leu Gly Thr Val Met Arg Ser Leu Gly Gln  
                             290                            295                            300  
 aac cca acg gaa gca gaa ttg cag gat atg atc aat gaa gtc gat gct 960  
 Asn Pro Thr Glu Ala Glu Leu Gln Asp Met Ile Asn Glu Val Asp Ala  
 305                            310                            315                            320  
 gat ggc aat gga acg att tac ttt cct gaa ttt ctt act atg atg gct 1008  
 Asp Gly Asn Gly Thr Ile Tyr Phe Pro Glu Phe Leu Thr Met Met Ala  
                             325                            330                            335  
 aga aaa atg aag gac aca gac agc gaa gag gaa atc cga gaa gca ttc 1056  
 Arg Lys Met Lys Asp Thr Asp Ser Glu Glu Glu Ile Arg Glu Ala Phe  
                             340                            345                            350  
 cgt gtt ttt gac aag gat ggg aac ggc tac atc agc gct gct gaa tta 1104  
 Arg Val Phe Asp Lys Asp Gly Asn Gly Tyr Ile Ser Ala Ala Glu Leu  
                             355                            360                            365  
 cgt cac gtc atg aca aac ctc ggg gag aag tta aca gat gaa gaa gtt 1152  
 Arg His Val Met Thr Asn Leu Gly Glu Lys Leu Thr Asp Glu Glu Val  
                             370                            375                            380  
 gat gaa atg ata agg gaa gca gat atc gat ggt gat ggc caa gta aac 1200

Asp Glu Met Ile Arg Glu Ala Asp Ile Asp Gly Asp Gly Gln Val Asn  
 385 390 395 400  
 tat gaa gag ttt gta caa atg atg aca gca aag 1233

Tyr Glu Glu Phe Val Gln Met Met Thr Ala Lys  
 405 410

<210> 57

<211> 288

<212> PRT

<213> *Montipora. sp*

<400> 57.

Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr  
 1 5 10 15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp  
 20 25 30

Pro Lys Arg Arg Trp Lys Lys Asn Phe Ile Ala Val Ser Ala Ala Asn  
 35 40 45

Arg Phe Lys Lys Ile Ser Ser Ser Gly Ala Leu Gly Gly Gly Gly Ser  
 50 55 60

Glu Leu Met Val Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr  
 65 70 75 80

Met Ser Gly Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly  
 85 90 95

Lys Gly Lys Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr  
 100 105 110

Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Leu Phe  
 115 120 125

Gln Tyr Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp

130	135	140	
Tyr Val Lys Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Thr Met			
145	150	155	160
Asn Phe Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile			
	165	170	175
Gln Gly Asn Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Thr Asn Phe			
	180	185	190
Pro Pro Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro			
	195	200	205
Ser Thr Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp			
	210	215	220
Tyr Met Ala Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe			
225	230	235	240
Lys Ser Thr Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His			
	245	250	255
Tyr Ile Asp Arg Lys Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr			
	260	265	270
Ser Val Glu Gln Cys Glu Ile Ala Ile Ala Arg His Ser Leu Leu Gly			
	275	280	285

<210> 58

<211> 864

<212> DNA

<213> *Montipora. sp*

<400> 58

atg cgg ggt tct cat cat cat cat cat cat ggt atg gct agc atg act 48

Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr

1

5

10

15



ggt gga cag caa atg ggt cgg gat ctg tac gac gat gac gat aag gat 96  
 Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp  
                   20                                  25                                  30  
 ccc aag agg cgc tgg aag aaa aac ttc att gcc gtc agc gct gcc aac 144  
 Pro Lys Arg Arg Trp Lys Lys Asn Phe Ile Ala Val Ser Ala Ala Asn  
                   35                                  40                                  45  
 cgg ttc aag aag atc tcc agc tcc ggg gca ctg gga ggt gga ggt agt 192  
 Arg Phe Lys Lys Ile Ser Ser Ser Gly Ala Leu Gly Gly Gly Gly Ser  
                   50                                  55                                  60  
 gag ctc atg gtg agt gtg atc gct aaa caa atg acc tac aag gtt tat 240  
 Glu Leu Met Val Ser Val Ile Ala Lys Gln Met Thr Tyr Lys Val Tyr  
                   65                                  70                                  75                                  80  
 atg tca ggc acg gtc aat gga cac tac ttt gag gtc gaa ggc gat gga 288  
 Met Ser Gly Thr Val Asn Gly His Tyr Phe Glu Val Glu Gly Asp Gly  
                                   85                                  90                                  95  
 aaa gga aag cct tac gag gga gag cag aca gta aag ctc act gtc acc 336  
 Lys Gly Lys Pro Tyr Glu Gly Glu Gln Thr Val Lys Leu Thr Val Thr  
                   100                                  105                                  110  
 aag ggt gga cct ctg cca ttt gct tgg gat att tta tca cca ctg ttt 384  
 Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Leu Phe  
                   115                                  120                                  125  
 cag tac gga agc ata cca ttc acc aag tac cct gaa gac atc cct gat 432  
 Gln Tyr Gly Ser Ile Pro Phe Thr Lys Tyr Pro Glu Asp Ile Pro Asp  
                   130                                  135                                  140  
 tat gta aag cag tca ttc cct gag gga tat aca tgg gag agg acc atg 480  
 Tyr Val Lys Gln Ser Phe Pro Glu Gly Tyr Thr Trp Glu Arg Thr Met  
                   145                                  150                                  155                                  160

aac ttt gaa gat ggt gca gtg tgt act gtc agc aat gat tcc agc atc 528  
 Asn Phe Glu Asp Gly Ala Val Cys Thr Val Ser Asn Asp Ser Ser Ile  
                     165                    170                    175  
 caa ggc aac tgt ttc atc tac aat gtc aaa atc tct ggt acg aac ttt 576  
 Gln Gly Asn Cys Phe Ile Tyr Asn Val Lys Ile Ser Gly Thr Asn Phe  
                     180                    185                    190  
 cct ccc aat gga cct gtt atg cag aag aag aca cag ggc tgg gaa ccc 624  
 Pro Pro Asn Gly Pro Val Met Gln Lys Lys Thr Gln Gly Trp Glu Pro  
                     195                    200                    205  
 agc act gag cgt ctc ttt gca cga gat gga atg ctg ata gga aac gat 672  
 Ser Thr Glu Arg Leu Phe Ala Arg Asp Gly Met Leu Ile Gly Asn Asp  
                     210                    215                    220  
 tat atg gct ctg aag ttg gaa gga ggt ggt cac tat ttg tgt gaa ttt 720  
 Tyr Met Ala Leu Lys Leu Glu Gly Gly Gly His Tyr Leu Cys Glu Phe  
 225                    230                    235                    240  
 aaa tct act tac aag gca aag aag cct gtg agg atg cca ggg tat cac 768  
 Lys Ser Thr Tyr Lys Ala Lys Lys Pro Val Arg Met Pro Gly Tyr His  
                     245                    250                    255  
 tat att gac cgc aaa ctg gat gta acc agt cac aac agg gat tac aca 816  
 Tyr Ile Asp Arg Lys Leu Asp Val Thr Ser His Asn Arg Asp Tyr Thr  
                     260                    265                    270  
 tct gtt gag cag tgt gaa ata gcc att gca cgc cac tct ttg ctc ggt 864  
 Ser Val Glu Gln Cys Glu Ile Ala Ile Ala Arg His Ser Leu Leu Gly  
                     275                    280                    285

<210> 59

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 59

ccagagatga agatgaggta ctacatggac ggc 33

<210> 60

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 60

catgagttca caattgaagg tgaaggc 27

<210> 61

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 61

gaaggcacag gcagacctta cgaggga 27

<210> 62

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 62

ccaatgcctt tcgcgtttga cttagtg

27

<210> 63

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 63

ttagtgtcac acgtgttctg ttacggc

27

<210> 64

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 64

gaaaggtcgt tggagttcga agatggt

27

<210> 65

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 65

gaagatggtg ggtccgcttc agtcagtgcg

30

<210> 66

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 66

agccttagag gaaacacctt ctaccacaaa tcca 34

<210> 67

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 67

caaatccaaa ttactgggg ttaactttcc tg 32

<210> 68

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 68

gccgatggtc ctatcatgca aaaccaaagt 30

<210> 69

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 69

gccgatggtc ctatcatgca aaaccaaagt gttgattggg agcca 45

<210> 70

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 70

gagaaaatta ctgccagcga cggagttctg aag 33

<210> 71

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 71

gatgttacga tgtacctaaa acttgaagga ggcggcaatc ac 42

<210> 72

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 72

cttaaaatgc caggaagcca ttacatcagc catcgctcg tcagg 45

<210> 73

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 73

gatgcagtag ctcatccct cgagcaccac cacc 34

<210> 74

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 74

gaaggrtgyg tcaayggrca y 21

<210> 75

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 75

acvggdcat ydgvaagaaa rtt 23

<210> 76

<211> 36

<212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Description of Artificial Sequence: Synthetic DNA  
 <400> 76  
 ggccacgcgt cgactagtac gggiigggii gggiig 36  
 <210> 77  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Description of Artificial Sequence: Synthetic DNA  
 <400> 77  
 ctcagggaat gactgcttta cat 23  
 <210> 78  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Description of Artificial Sequence: Synthetic DNA  
 <400> 78  
 ggccacgcgt cgactagtac 20  
 <210> 79  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
 <220>



<223> Description of Artificial Sequence: Synthetic DNA

<400> 79

gtcttcaggg tacttggtga 20

<210> 80

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 80

atgtaaagca gtcattccct gag 23

<210> 81

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 81

cccgatccg accatggcta ccttggttaa aga 33